

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model
Run on: May 22, 2006, 19:21:50 ; Search time 6639 Seconds
(without alignments)
11327.334 Million cell updates/sec
Title: US-10-626-445-5
Perfect score: 1176
Sequence: 1 agtgcgagctcaacagtagc.....accagtcagtagctttcttga 1176
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sy.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_hcg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1176	100.0	1538	6	AF358859	Mus muscu
2	958.4	81.5	1593	6	AF358860	Rattus no
3	838	71.3	1308	6	BC111862	Mus muscu
4	821.4	69.8	199837	6	AC131672	Mus muscu
5	686.6	58.4	1173	2	AR142850	Sequence
6	686.6	58.4	1173	2	BD015847	Novel pol
7	686.6	58.4	1173	2	CS173186	Sequence
8	686.6	58.4	1173	2	CS178018	Sequence
9	686.6	58.4	1173	2	AR391860	Sequence
10	686.6	58.4	1173	2	AX109119	Sequence
11	686.6	58.4	1173	2	AX139113	Sequence
12	686.6	58.4	1173	5	AF325356	Homo sapi
13	686.6	58.4	1173	5	AF329449	Homo sapi
14	686.6	58.4	1173	5	AY008280	Homo sapi
15	686.6	58.4	1173	5	AY136745	Homo sapi
16	686.6	58.4	1173	5	HS298292	Homo sapi
17	686.6	58.4	1266	2	AX376577	Sequence
18	686.6	58.4	1300	2	AX301229	Sequence

19	586.6	58.4	1312	2	BD095598	BD095598 Novel gua
20	586.6	58.4	1312	5	AB045370	AB045370 Homo sapi
21	586.6	58.4	1316	5	BC069136	BC069136 Homo sapi
22	586.6	58.4	1847	5	BC112348	BC112348 Homo sapi
23	586.6	58.4	3689	2	AX549343	AX549343 Sequence
24	586.6	58.4	3689	5	AF312230	AF312230 Homo sapi
25	685	58.2	1227	2	BD097512	BD097512 Novel gua
26	685	58.2	1285	5	AB044934	AB044934 Homo sapi
27	683.4	58.1	1173	2	AX301763	AX301763 Sequence
28	683.4	58.1	1173	5	AF307973	AF307973 Homo sapi
29	677	57.6	1175	5	AB189711	AB189711 Macaca fa
30	651	55.4	236694	12	AC118386	AC118386 Rattus no
31	621.4	52.8	1291	14	AB053300	AB053300 Sus scrof
32	613	52.1	1451	6	AF358858	AF358858 Cavia por
33	442	37.6	140555	5	AC007922	AC007922 Homo sapi
34	442	37.6	166206	12	AC009668	AC009668 Homo sapi
35	442	37.6	167296	12	AP002507	AP002507 Homo sapi
36	442	37.6	169144	5	AC090244	AC090244 Homo sapi
37	442	37.6	184938	12	AP002476	AP002476 Homo sapi
38	442	37.6	193779	12	AP001327	AP001327 Homo sapi
39	371	31.5	1950	2	CQ947118	CQ947118 Sequence
40	284.4	24.2	528	5	AY561469	AY561469 Pan trogl
41	283.8	24.1	522	5	AY561470	AY561470 Gorilla g
42	271.6	23.1	1326	2	AX451922	AX451922 Sequence
43	270.6	23.0	429	2	CQ727333	CQ727333 Sequence
44	178	15.1	1249	6	AF267538	AF267538 Cavia por
45	172.8	14.7	1239	2	E39806	E39806 Novel guano

ALIGNMENTS

RESULT 1
AF358859
LOCUS Mus musculus histamine H4 receptor mRNA, complete cds.
DEFINITION AF358859 1538 bp mRNA linear ROD 02-SEP-2001
ACCESSION AF358859
VERSION AF358859.1 GI:15420534
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1538)
AUTHORS Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1538)
AUTHORS Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
FEATURES
Location/Qualifiers
1..1538
/organism="Mus musculus"
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Qy	181	GACTTCCTCGTGGG	TTTGATTTTCATTTCCCTCTGTACATCCCTCAGCTGTGTGTTAACTGG	240						
Db	241	GACTTCCTCGTGGG	TTTGATTTTCATTTCCCTCTGTACATCCCTCAGCTGTGTGTTAACTGG	300						
Qy	241	AATTTTGGAGTGGAA	TCGTGCAATGTTTTGGCTCAATTACTGACTATCTTTTGTGCAACGCCA	300						
Db	301	AATTTTGGAGTGGAA	TCGTGCAATGTTTTGGCTCAATTACTGACTATCTTTTGTGCAACGCCA	360						
Qy	301	TCGTGCTACAAATAT	TGTCCCTCATTAGCTACGATCGATACGATCCAGTCAGTTTCAAAATGCTGTG	360						
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Qy	361	TCCTTATAGGGCT	CAAACACATCGGCATCATGAAGATTGTGCTCAAAATGGGCTGTGTTGG	420						
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Qy	421	ATACTGCTTTCTTGG	TAAATGGCCGATGATTCGTGCTTCAGATTCGTGGAAGAAACAGC	480						
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Qy	481	ACGAACAACAAAGG	ACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCCCTCACCATTACA	540						
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Qy	601	TGGAGCCTGTGGA	ACGCTAGGGCTCTCAGTAGGTGCCCTAGCCATGTGGAATTCCTCCACT	660						
Db	661	TGGAGCCTGTGGA	ACGCTAGGGCTCTCAGTAGGTGCCCTAGCCATGTGGAATTCCTCCACT	720						
Qy	661	ACCTCTTCCAGTGT	CTTACAGACATTTACAGAGCTGGGTGGCTTCGACGACAAAGTAAT	720						
Db	721	ACCTCTTCCAGTGT	CTTACAGACATTTACAGAGCTGGGTGGCTTCGACGACAAAGTAAT	780						
Qy	721	CCTGGATTGAAGAA	TACAGCTGCACTCTGTGCTTCTCGAAGAAAGCAGCAGC	780						
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Qy	781	ATCCTGTGTCTTAA	GGACTCACATGAACACAGCATATCACTGCCCTTTCAAAGTGGGTTC	840						
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Qy	901	AGGAAGCTTAGCAG	GTCACTGGCCATCTCTCTGACGCTTTTGGCATTTGCTGGGCTCCA	960						
Db	961	AGGAAGCTTAGCAG	GTCACTGGCCATCTCTCTGACGCTTTTGGCATTTGCTGGGCTCCA	1020						
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Qy	1021	TGTTACAGCAATTCGCTTCTGGCTGCAATGGTTTCAATTCGTTGTGTTAATCCCTTCTGTAC	1080
Db	1081	TGTTACAGCAATTCGCTTCTGGCTGCAATGGTTTCAATTCGTTGTGTTAATCCCTTCTGTAC	1140
Qy	1081	CTTTTGTGTACAGGCGCTTTCAGAGAGCGCTTTCGGAAGATACATCTTGTGTGACAAAGCAA	1140
Db	1141	CTTTTGTGTACAGGCGCTTTCAGAGAGCGCTTTCGGAAGATACATCTTGTGTGACAAAGCAA	1200
Qy	1141	CCAGCGCTGTCCAGACACCAAGTCAGTATCTTCTTGA	1176
Db	1201	CCAGCGCTGTCCAGAACCAAGTCAGTATCTTCTTGA	1236
RESULT 2			
AF358860		1593 bp	mRNA linear ROD 02-SEP-2001
LOCUS			
DEFINITION			Rattus norvegicus histamine H4 receptor mRNA, complete cds.
ACCESSION			AF358860
VERSION			AF358860.1 GI:15420536
KEYWORDS			
SOURCE			Rattus norvegicus (Norway rat)
ORGANISM			Rattus norvegicus
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
AUTHORS			1 (bases 1 to 1593)
TITLE			Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
JOURNAL			Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation
REFERENCE			Unpublished
AUTHORS			2 (bases 1 to 1593)
TITLE			Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
JOURNAL			Direct Submission
FEATURES			Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA
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			/strain="Sprague-Dawley"
			/db_xref="taxon:10116"
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			/note="G-protein-coupled receptor"
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ORIGIN			
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Qy	61	TTAATGTCCTTCATTTGGCTTTTGCTATAAATGGTAGGCAATGCTGTGGTCACTTTAGCCTTT	120
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Db 216 GACTTCTTCTGCGGTGTCTCCATCTCCTCTGTACATCCCTCAGCTGTTTAACTCG 275
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Db 816 CTCTGTGCTTCTTAAAGCTCAGATCAATGAGCAGTATCATCTGCTTCAAGTGGGTTC 875
Qy 841 TTCTGCGGATCGGAAAGTGGAGCGCTTCCGCAAGGAGTACGAGAGCTTCTCAGAGGC 900
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Db 1056 TGGTACAGCATGCTTCTGCTGCAATGTTTCAATTCGTTTGTATTCCTTCTCTGATC 1115
Qy 1081 CTTTGTGTCCAGCGCTTTCCAGAGGCTTTCTGGAAGTACTTTTGTGTGACAAAGCAA 1140
Db 1116 CTTTGTGTCCAGAGCTTTCCAGAGGCTTTCTGGAAGTACTTTCTGTGTGACAAAGCAA 1175
Qy 1141 CCAGCGCTGTCCAGAAACCAAGTCAAGTATCTTTGA 1176
Db 1176 CCAGCACTTCCAGAGCCAGTCAAGTATCTTTGA 1211

RESULT 3
BC111862

LOCUS
DEFINITION
MUS musculus histamine H4 receptor, mRNA (cdna clone MGC:130500 IMAGE:40046148), complete cds.
BC111862
BC111862.1 GI:84993254
MGC.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1308)
REFERENCE
AUTHORS
Srausberg, R.L., Reingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquelliano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dutton, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1308)
NIH MGC Project
Direct Submission
Submitted (13-JAN-2006) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUM)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hagnighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., McDowell, J., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, B.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLUM at: <http://image.llnl.gov>
Series: IRAM Plate: 15 Row: c Column: 19.

FEATURES
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Clone identification sequence tag: GTGGTTA"

gene

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LQWFNSFVNPFLYPLCHRRFQKAPFKILCVTKQPALSQNSVSS"

ORIGIN

Query Match 71.3%; Score 838; DB 6; Length 1308;
Best Local Similarity 86.1%; Pred. No. 1.6e-277;
Matches 1012; Conservative 0; Mismatches 0; Indels 164; Gaps 1;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTT 60
DB 60 ATGTCGGAGTCTAACAGTACTGGCATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTT 119
QY 61 TTAATGTCCTCATTTGCTTTGCTATTAATGGTAGGCAATGCTGGTGCATCTTTAGCCCTTT 120
DB 120 TTAATGTCCTCATTTGCTTTGCTATTAATGGTAGGCAATGCTGGTGCATCTTTAGCCCTTT 179
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTCTTAATTTGGCTATTTCT 180
DB 180 GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTCTTAATTTGGCTATTTCT 239
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DB 240 GACTTCTCTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGGTGTTTAACTGG 252
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DB 253 -----GTG 255
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QY 421 ATACTGGCTTTCTTGTGTAATGGCCCATGATTTCTGGCTTCAGATTTCTTGAAGAAGCAGC 480
DB 316 ATACTGGCTTTCTTGTGTAATGGCCCATGATTTCTGGCTTCAGATTTCTTGAAGAAGCAGC 375
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AC131672/LOCUS 199837 bp DNA linear ROD 11-FEB-2004
DEFINITION Mus musculus chromosome UNK clone RP23-314021, complete sequence.
AC131672
ACCESSION AC131672.3 GI:42517281
VERSION HTG.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 Wilson, R.K.
AUTHORS The sequence of Mus musculus clone
TITLE Unpublished
JOURNAL 2 (bases 1 to 199837)
REFERENCE 2 McPherson, J.D. and Waterston, R.H.
AUTHORS Direct Submission
TITLE Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
JOURNAL Parkway, St. Louis, MO 63108, USA
REFERENCE 3 Wilson, R.K.
AUTHORS Direct Submission
TITLE Submitted (06-NOV-2003) Genome Sequencing Center, 4444 Forest Park
JOURNAL Parkway, St. Louis, MO 63108, USA
REFERENCE 4 Wilson, R.K.
AUTHORS Direct Submission
TITLE Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest Park
JOURNAL Parkway, St. Louis, MO 63108, USA
REFERENCE 5 Wilson, R.K.
AUTHORS Direct Submission
TITLE Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest Park
JOURNAL Parkway, St. Louis, MO 63108, USA
COMMENT On Feb 11, 2004 this sequence version replaced gi:38194370.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Project Information -----

Center project name: M_BA0314021

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Query Match 69.8%; Score 821.4; DB 6; Length 199837;
Best Local Similarity 95.9%; Pred. No. 3.4e-271; Indels 0; Gaps 0;
Matches 843; Conservative 0; Mismatches 36;

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Qy 418 TGGATCTGCTTTCTTGGTAAATGGCCCGATGATCTGGCTTCAGATTCTTGGAAAGAC 477
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Qy 598 TACTGAGCCTGTGGAAGCTGAGGCTCTCAGTAGTGCCCTAGCCATGCTGCATTTCTCC 657
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Qy 718 AATCTGGATTGAAGGAATCAGCTGCATCTGTCACCTCAGAAAGTCTCGAAAGAAAGAGC 777
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LOCUS ARI42850 1173 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6204017.
ACCESSION ARI42850
VERSION ARI42850.1 GI:15104136
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Unland,S.P. and Wang,S.
TITLE Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
FEATURES Location/Qualifiers
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Query Match 58.4%; Score 686.6; DB 2; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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RESULT 6
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LOCUS BD015847 1173 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide.
ACCESSION BD015847
VERSION BD015847.1 GI:22556984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Peter, B. and Olajale, M.A.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
COMMENT PFIZER INC
OS Homo sapiens (human)
PN JP 2001211889-A/1
PD 07-AUG-2001
PF 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641:4, 20-APR-2000 GB 0009973:9 PI
BR BEAT PETER, MARK ANTONY OLAYLEE
PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,
PC A61P11/00,
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PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/ PC
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PC C12P21/02, C12Q1/02, G01N33/15, G01N33/50, G01N33/53//C12P21/08,
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CC Novel polypeptide
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Query Match 58.4%; Score 686.6; DB 2; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATCTCGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCTCTTGGCAATTT 60
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 DEFINITION Sequence 13 from Patent EP1580271.
 ACCESSION CS173186
 VERSION CS173186.1 GI:77153219
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Hominidae; Homo.
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 Chen, R.
 HUMAN ORPHAN G PROTEIN-COUPLED RECEPTORS
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 JOURNAL Arena Pharmaceuticals, Inc. (US)
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 Query Match 58.4%; Score 686.6; DB 2; Length 1173;
 Best Local Similarity 75.1%; Pred. No. 4.1e-225;
 Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

 Qy 1 ATGTCGGAGTCTAACAGTACTGTCATCTTGCACACGCTGCTCAGTCCCTTGGCATTT 60
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 DEFINITION Sequence 13 from Patent EP1584683.
 ACCESSION CS178018
 VERSION CS178018.1 GI:77733617
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Hominidae; Homo.
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 Chen, R.
 HUMAN ORPHAN G PROTEIN-COUPLED RECEPTORS
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 JOURNAL Arena Pharmaceuticals, Inc. (US)
 FEATURES Location/Qualifiers

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ORIGIN
Query Match      58.4%; Score 686.6; DB 2; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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DEFINITION Sequence 1 from patent US 6613533.
ACCESSION AR391860
VERSION AR391860.1 GI:40115588
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
Umland, S.P. and Wang, S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
Schering Corporation; Kenilworth, NJ
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ORIGIN
Query Match 58.4%; Score 686.6; DB 2; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGAGTCTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGGTCCTTGGCAATTT 60
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DEFINITION Sequence 1 from Patent WO0125432.
ACCESSION AX109119
VERSION AX109119.1 GI:13924093
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
Umland, S. and Wang, S.
TITLE Histamine receptor
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;
SCHERING CORPORATION (US)
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ORIGIN

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Query Match 58.4%; Score 686.6; DB 2; Length 1173;  
Best Local Similarity 75.1%; Pred. No. 4.le-225;  
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;  
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RESULT 11
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LOCUS AX139113 1173 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 1 from Patent EPI096009.
ACCESSION AX139113
VERSION AX139113.1 GI:14274791
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
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1 Peter, B. and O'Reilly, M.A.
G-protein coupled receptor-like polypeptide
Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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Query Match 58.4%; Score 686.6; DB 2; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Qy 1 ATGTCGAGTCTAACAGTACTGGCATCTGCGCACCGCTGTCAGGTCCTTGGCATTT 60
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DEFINITION Homo sapiens histamine receptor H4 (AXOR35) mRNA, complete cds.
ACCESSION AF325356
VERSION AF325356.1 GI:15553202
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
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1 (bases 1 to 1173)
Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K.B., Dytko, G.M.,
Mannan, I.J., Boyce, R., Alston, J., Tierney, L.A., Li, X.,
Herrity, N.C., Vawter, L., Sarau, H.M., Ames, R.S., Davenport, C.M.,
Hieble, P., Wilson, S., Bergsma, D.J. and Fitzgerald, L.R.
Cloning, expression, and pharmacological characterization of a
novel human histamine receptor
Mol. Pharmacol. 59 (3), 434-441 (2001)
JOURNAL
PUBMED 11179436
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REFERENCE 2 (bases 1 to 1173)
AUTHORS Zhu, Y., Michalovich, D. and Fitzgerald, L.R.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box 1539, King of Prussia, PA 19406, USA

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ORIGIN
Query Match 58.4%; Score 686.6; DB 5; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.1e-225;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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VERSION AF329449.1 GI:13876643
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Hominidae; Homo.
1 (bases 1 to 1173)
Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A.,
Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shan, N.,
Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M.
and Monsma, F.J. Jr.
Cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
11181941
2 (bases 1 to 1173)
Monsma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and
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Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
USA
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1 (bases 1 to 1173)			
Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K.,			
Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and			
O'Dowd, B.F.			
Discovery of a novel member of the histamine receptor family			
Mol. Pharmacol. 59 (3), 427-433 (2001)			
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2 (bases 1 to 1173)			
Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and			
O'Dowd, B.F.			
Discovery of H4, a Novel Histamine Receptor			
Unpublished			
3 (bases 1 to 1173)			
Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and			
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Direct Submission			
Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8			
Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada			
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REFERENCE			
AUTHORS Puhl,H.L., III, Ikeda,S.R. and Aronstam,R.S.			
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Institute, One Guthrie Square, Sayre, PA 18840, USA			
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 721 CTTGGATTGAAGGAATCAGCTGCAATCTGCTCACTCAGAAAGTCTCTGAAAGAAAGAGCAGC 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 715 TCTGCATCGACAGAAGTTCTCTGCACTCCTTCAITTCAGAGACAGAGAGAGAGAGTAGT 774
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 781 ATCTCTGTGCTCTTAAGGACTCACTGAACAGCAGATATCACTGCTTCAAAGTGGGTTCC 840
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 775 CTCATGTTTTCCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCAAAATGGGTTCC 834
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 841 TTCTGGCGATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC 900
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACAAAGGGNACATGTTGAACTGCTTAGAGCC 894
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 901 AGGAAGCTAGCCAGGTCACTGGCCATCCTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 960
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 895 AGGAGATTAGCCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTCTGGGCTCCA 954
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 961 TACTGTCTGTTCACAAATGTCTTCAACTTACCAGAAAGGAAAGCCCAAAATCGGTG 1020
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 955 TATTTCTGTTCACAAATTTGCTTCAATTTTATTTCTCAGCAACAGGTCCTAAAATCAGTT 1014
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1021 TGGTACAGCATTTGCTGCTGCAATGGTTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1015 TGGTATAGAAATTTGATTTGGCTTCAATTCCTTTGTCATCTCTTTTGTAT 1074
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1081 CCTTTGTGTCAAGCGCTTTCAGAAAGCTTTCTGGAAGATACCTTTGTGTACAAAGCAA 1140
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1075 CCAATGTGTCAAGCGCTTTCAGAAAGCTTCTTGAAGATATTTTGTATATAAAAAAGCAA 1134
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1141 CCAGCGCTGTCAAGAAC--CAGTCAAGTATCTTCTGA 1176
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1135 CCTCTACCATCACAAACAGTCGGTCAAGTATCTTCTTAA 1173
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 19:08:42 ; Search time 755 Seconds
(without alignments)
10860.085 Million cell updates/sec

Title: US-10-626-445-5
Perfect score: 1176
Sequence: 1 atgtcgagctcaacagctac.....accagtcagtattcttttga 1176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_8:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*
- 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1176	100.0	1176	6	Aai70981 Mouse his
2	1176	100.0	1538	12	Ado30257 Mouse GPC
3	958.4	81.5	1176	6	Aai70982 Rat hist
4	686.6	58.4	1173	3	Aaa46023 Human G p
5	686.6	58.4	1173	3	Aad01124 Human orp
6	686.6	58.4	1173	4	Aaf83203 Human GPC
7	686.6	58.4	1173	5	Aah24007 Human G p
8	686.6	58.4	1173	6	Abz80663 Human his
9	686.6	58.4	1173	6	Abq78739 Nucleotid
10	686.6	58.4	1173	6	Aai70980 Human his
11	686.6	58.4	1173	8	Acag3262 Human cdn
12	686.6	58.4	1173	10	Adg98759 Human orp
13	686.6	58.4	1173	10	Abss57063 Human cdn
14	686.6	58.4	1173	11	Adj26922 Human end
15	686.6	58.4	1173	12	Adg86374 Human end
16	686.6	58.4	1173	12	Adj88375 Novel hum
17	686.6	58.4	1173	12	Adp20167 Human G p
18	686.6	58.4	1173	12	Adq75073 Human cdn

19	686.6	58.4	1173	14	Adv43700 Human psy
20	686.6	58.4	1173	14	Ady86899 Human his
21	686.6	58.4	1266	6	Abk12959 DNA seque
22	686.6	58.4	1300	6	AbA02496 Human G p
23	686.6	58.4	1312	4	Aah47911 Human G p
24	686.6	58.4	3689	8	Abz42573 Human his
25	686.6	58.4	3689	12	Ado05719 Human his
26	686.6	58.4	3689	12	Ado29967 Human GPC
27	685.2	58.3	1170	9	Aad55126 Human H4
28	685	58.2	1227	4	Aai66009 Human GPR
29	685	58.2	1265	6	Aae98078 Human DNA
30	685	58.2	1265	9	Aad55125 Human H4
31	683.4	58.1	1173	6	Aai67750 Human his
32	613	52.1	1170	6	Aai70983 Guinea pi
33	505.8	43.0	1166	9	Aad55124 Human H4
34	436.6	37.1	1103	9	Aad55123 Human H4
35	371	31.5	1950	13	Adu82889 Ligand up
36	271.6	23.1	1326	6	Aad37667 Human G-p
C	269	22.9	540	6	Aas98150 Human DNA
38	172.8	14.7	1239	2	Aax84570 G-protein
39	172.8	14.7	1239	3	Aaa70639 Rat G-pro
40	172.8	14.7	2700	2	Aax84571 G-protein
41	172.8	14.7	2700	3	Aaa70640 Rat G-pro
42	171.6	14.6	1311	9	Aal59979 Human H3
43	168.6	14.3	1203	9	Aal59985 Human H3
44	145.4	12.4	1338	12	Adf66834 Murine hi
45	145.4	12.4	18105	8	Abz82337 Mouse his

ALIGNMENTS

RESULT 1

AAI70981
ID AAI70981 standard; cdna; 1176 BP.

XX AAI70981;

XX 18-MAR-2002 (first entry)

XX Mouse histamine H4 receptor cDNA.

XX Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
XX antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
XX diagnosis; gene therapy; ss.

XX Mus musculus.

XX WO200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WFI; 2002-114339/15.

XX P-PSDE; AAM50565.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
XX the proteins, useful in gene therapy for treating diseases where it is
XX beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 4; Fig 5A; 92pp; English.

XX The present sequence is that of a cDNA clone encoding a murine histamine
XX receptor of the H4 subtype. The cDNA was isolated from a mouse spleen
XX cDNA library. It shows 72.8% homology to the human H4 receptor coding
XX region. The invention provides mammalian (human, mouse, rat and guinea

PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 1360; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridize to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIP0 at
CC ftp.wipo.int/pub/published_pcr_sequences.

XX Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;

Query Match 100.0%; Score 1176; DB 12; Length 1538;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAAGCTGCTCAGTCCCTTGGCATTT 60
DB 61 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAAGCTGCTCAGTCCCTTGGCATTT 120
QY 61 TTAATGCTTCATTTGGCTTTGCTATAATGGTAGGCAATGCTGTGTCATCTTAGCCCTTT 120
DB 121 TTAATGCTTCATTTGGCTTTGCTATAATGGTAGGCAATGCTGTGTCATCTTAGCCCTTT 180
QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTCTTAATTTGGCTATTCT 180
DB 181 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATTTTTCTTAATTTGGCTATTCT 240
QY 181 GACTTCCTCGTGGGTTGATTTCCATTCCTCTGTAATCCCTCAGTGTGTTAACTGG 240
DB 241 GACTTCCTCGTGGGTTGATTTCCATTCCTCTGTAATCCCTCAGTGTGTTAACTGG 300
QY 241 AATTTTGGAGTGGATCTGCATGTTTGGCTCATTTACTGACTATCTTTGTGTCACCGCA 300
DB 301 AATTTTGGAGTGGATCTGCATGTTTGGCTCATTTACTGACTATCTTTGTGTCACCGCA 360
QY 301 TCTGTCTACAATATGTCCTCATTTAGCTACGATCGATACCAAGTCAGTTCCTCAAAATGCTGTG 360
DB 361 TCTGTCTACAATATGTCCTCATTTAGCTACGATCGATACCAAGTCAGTTCCTCAAAATGCTGTG 420
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTCCTCAAAATGGTGGCTGTTTGG 420
DB 421 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTCCTCAAAATGGTGGCTGTTTGG 480
QY 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGACAGC 480

DB 481 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGAAAGACAGC 540
QY 481 ACGAACACAAAGAGCATGTGAGCCTGGCTTTGTTTACAGAGTGGTACATCCTCACCATTACA 540
DB 541 ACGAACACAAAGAGCATGTGAGCCTGGCTTTGTTTACAGAGTGGTACATCCTCACCATTACA 600
QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
DB 601 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 660
QY 601 TGAGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGATTTCTCCACT 660
DB 661 TGAGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGATTTCTCCACT 720
QY 661 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
DB 721 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 780
QY 721 CCTGGATTGAGGAATCAGCTGCTCATCTGCTCAGTACAGAAATGCTCGAAGAAAGACGAGC 780
DB 781 CCTGGATTGAGGAATCAGCTGCTCATCTGCTCAGTACAGAAATGCTCGAAGAAAGACGAGC 840
QY 781 ATCTGTGTCTCTTAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840
DB 841 ATCTGTGTCTCTTAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 900
QY 841 TTCTGGCGATTCGAAAGTGCAGCGCTTCGCCAAAGGAGTACGACAGCTTCTCAGAGGC 900
DB 901 TTCTGGCGATTCGAAAGTGCAGCGCTTCGCCAAAGGAGTACGACAGCTTCTCAGAGGC 960
QY 901 AGAAGCTAGCAGGTCAGTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 960
DB 961 AGAAGCTAGCAGGTCAGTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 1020
QY 961 TACTGTCTGTTCACAATTTGCTTTTCAACTTACCCAGAAAGGAGTACGACAGCTTCTCAGAGGC 1020
DB 1021 TACTGTCTGTTCACAATTTGCTTTTCAACTTACCCAGAAAGGAGTACGACAGCTTCTCAGAGGC 1080
QY 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGTTCAATTCGTTTGTATTCCTTTCTGTAC 1080
DB 1081 TGGTACAGCATTTGCTTCTGGCTGCAATGTTCAATTCGTTTGTATTCCTTTCTGTAC 1140
QY 1081 CTTTGTGTGTCACAGGCTTTTCAGAAAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
DB 1141 CTTTGTGTGTCACAGGCTTTTCAGAAAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1200
QY 1141 CCAGCGCTGTTCACAGAACGAGTCAGTATCTTCTTGA 1176
DB 1201 CCAGCGCTGTTCACAGAACGAGTCAGTATCTTCTTGA 1236

RESULT 3

AAI70982

ID AAI70982 standard; cDNA; 1176 BP.

XX AAI70982;

XX AC

XX DT

XX 18-MAR-2002 (first entry)

XX DE

XX Rat histamine H4 receptor cDNA.

XX KW

XX Histamine H4 receptor; rat; antiasthmatic; antiallergenic;
XX antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
XX diagnosis; gene therapy; ss.

XX OS

XX Rattus rattus.

XX XX

XX WO200192485-A1.

XX PN

XX 06-DEC-2001.

XX XX

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.
PR (ORTH) ORTHO-MCNEIL PHARM INC.
PA
XX
XX
PI Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
DR P-PSDB; AAM50566.
XX
XX
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX
PS Claim 4; Fig 5C; 92pp; English.
XX
XX The present sequence is that of a cDNA clone encoding a rat histamine
CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA
CC library. It shows 72.5% homology to the human H4 receptor coding region.
CC The invention provides mammalian (human, mouse, rat and guinea pig)
CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC recombinant host cells that produce active recombinant protein. The
CC pharmacology of known histamine ligands is demonstrated. Mammalian
CC histamine H4 receptor may be used in gene therapy for the treatment of
CC diseases where it is beneficial to elevate mammalian histamine H4
CC receptor activity. Recombinant protein is useful for identifying
CC modulators of the mammalian histamine H4 receptor. Such modulators may be
CC useful for diagnosing, treating or preventing asthma, allergy,
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
CC disorders of the neuroendocrine system, stress and spasticity
XX
SQ Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;

Query Match 81.5%; Score 958.4; DB 6; Length 1176;
Best Local Similarity 88.4%; Pred. No. 2e-289;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTGGAGCTAACAGTACTGGCATCTTGGCCACCAGCTGCTCAGGTCCCTGGCATTTT 60
DB 1 ATGTGGAGCTAACGGCACTGACGCTTGGCCACTGCTCAGGTCCCTGGCATTTT 60
QY 61 TTAATGCTTTCATTTGCTTTGCTATTAATGCTAGGCAATGCTGGTCATCTAGCCCTT 120
DB 61 TTAATGCTTTCATTTGCTTTGCTATTAACGATAGGCAATGCTGGTCATTTAGCCCTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180
DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180
QY 181 GACTTCCTGGGGTTTGAATTCATTCCTCTGTGATACCCCTACGCTGTTTAACTGG 240
DB 181 GACTTCCTGGGGTGTGATCTCCATTCCTCTGTATACCTCCTCACAGCTGTTTAACTGG 240
QY 241 AATTTTGGAGTGAATCTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 AATTTTGGAGTGAATCTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 TCTGCTACAAATATGTCCTCATTAGCTACGATCGATACGATGCTGCTGCTGCTGCTGCTG 360
DB 301 TCGGCTACAGTATTGTCCTCATTAGCTACGATCGATACGATGCTGCTGCTGCTGCTGCTG 360
QY 361 TCTTATAGGGCTAACACATCGGATCACTGAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 CGTTATAGAGCAGACACACTGGCATCTGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 ATACTGGCTTCTTGGTAAATGGCCCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 ACGAAACAAGGACTGTGAGCCCTGGCTTTGTATACAGAGTGGTACATCCTCACCATTTACA 540

DB 481 ACCAACACAGAGAGTGCAGAGCCTTGGCTTTGTTACTGTAGTGGTACATCCTCGCATTTACA 540
QY 541 ATGCTCTTGAATTCCTGTCTTCTGTCTCATCTCTGTGTGCTTATTTCAATGTACAGATTTAC 600
DB 541 GCATTTCTTGAATTCCTGTCTTCTGTCTCATCTCTGTGTGCTTATTTCAATGTACAGATTTAC 600
QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGATTTCTCCACT 660
DB 601 TGGAGCCTGTGGAAGCGTAGGGAGTCTCAGTAGGTGCCCTAGCCATGCTGATTTCTCCACT 660
QY 661 ACCTTCTCAGTCTTTCAGGACACTTACACAGAGCTGGGTGGCTTGCAGGACAAAGTAAT 720
DB 661 ACCTTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTGGCTTGTAGGACAAAGTCTT 720
QY 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCCGAAAGAGCAGC 780
DB 721 CCTGGATTGAAGGAACCCAGCCGATCCCTTCATTCAGAAAGTCCACGAGGAAGAGCAGT 780
QY 781 ATCTGTGTCTTAAAGGACTCAGATGAACAGCAGATATCACTGCTTCAAAGTGGGTTC 840
DB 781 CTCTGTGTCTTAAAGGACTCAGATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
QY 841 TTCTGGGATCGGAAGTGTGAGCGCTTCCGCCAAGGGAGTACGAGAGCTTCTCAGAGGC 900
DB 841 TTCTGGCGATCAGAAAGCCAGTCTTCCACGAGAGAGCAGCCTGGAGCTTCTCAGAGGC 900
QY 901 AGGAAGCTAGCAGGTACCTGCGCATCTTCTGAGGCTTTTGGCATTTGCTGGGCTCCA 960
DB 901 AGGAAGCTAGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 TACTGTCTGTTCACAAATGTCTTCAACTTACCAGAACCGAACCCCAATCGGTG 1020
DB 961 TATTGCTGTTCACAAATGTCTTCAACTTATTCGACAGAGGGAGCGCCCAATCGATT 1020
QY 1021 TGGTACAGCATTCGCTTGGCTGCAATGGTTCATTCGTTGTTGTTAATCCCTTCTGTAC 1080
DB 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAAATTCACCTTATTAATCCCTTCTATAC 1080
QY 1081 CTTTGTGTACAGAGGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGCTGTGACAAAGCAA 1140
DB 1081 CTTTGTGTACAGAGGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGCTGTGACAAAGCAA 1140
QY 1141 CCAGCGCTGTACAGAACCAAGTCAAGTATCTTCTTGA 1176
DB 1141 CCAGCACTTACAGACCCAGTCAAGTATCTTCTTGA 1176

RESULT 4
ID AAA46023
AC AAA46023;
XX
XX 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hrup7 encoding cDNA SEQ ID NO:13.
XX
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;
XX ss.
OS Homo sapiens.
XX
XX WO200022131-A2.
XX
XX 20-APR-2000.
XX
XX 13-OCT-1999; 99WO-US024065.
XX
XX 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.

PR	16-FEB-1999;	99US-0120416P.	
PR	26-FEB-1999;	99US-0121852P.	
PR	12-MAR-1999;	99US-0123944P.	
PR	12-MAR-1999;	99US-0123945P.	
PR	12-MAR-1999;	99US-0123946P.	
PR	12-MAR-1999;	99US-0123948P.	
PR	12-MAR-1999;	99US-0123949P.	
PR	12-MAR-1999;	99US-0123951P.	
PR	28-MAY-1999;	99US-0136436P.	
PR	28-MAY-1999;	99US-0136437P.	
PR	28-MAY-1999;	99US-0136439P.	
PR	28-MAY-1999;	99US-0137127P.	
PR	28-MAY-1999;	99US-0137131P.	
PR	28-MAY-1999;	99US-0137567P.	
PR	29-JUN-1999;	99US-0141448P.	
PR	27-AUG-1999;	99US-0151114P.	
PR	03-SEP-1999;	99US-0152524P.	
PR	29-SEP-1999;	99US-0156555P.	
PR	29-SEP-1999;	99US-0156633P.	
PR	29-SEP-1999;	99US-0156634P.	
PR	29-SEP-1999;	99US-0156653P.	
PR	01-OCT-1999;	99US-0157280P.	
PR	01-OCT-1999;	99US-0157281P.	
PR	01-OCT-1999;	99US-0157282P.	
PR	01-OCT-1999;	99US-0157293P.	
PR	01-OCT-1999;	99US-0157294P.	
PR	12-OCT-1999;	99US-00416760.	
PR	12-OCT-1999;	99US-00417044.	
XX			
PA	(AREN-) ARENA PHARM INC.		
XX			
PI	Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;		
PI	Gore M, Liaw CW, Lin I, Lowitz K, White C;		
XX			
DR	WPI; 2000-317986/27.		
DR	P-PSDB; AAB02831.		
XX			
PT	Non-endogenous, human G protein-coupled receptors for screening receptor,		
PT	inverse or partial agonists useful as therapeutic agents.		
XX			
PS	Example 1; Page 88-89; 187pp; English.		
XX			
CC	The present invention describes transmembrane receptors, preferably human		
CC	G protein coupled receptors (GPCR), for which the endogenous ligand is		
CC	unknown (orphan GPCR receptors). More specifically the present invention		
CC	relates to non-endogenous, constitutively activated versions of a human		
CC	GPCR. These non-endogenous human GPCRs can be useful for the direct		
CC	identification of candidate compounds as receptors agonists, inverse		
CC	agonists or partial agonists for use as pharmaceutical agents. AAA46017		
CC	to AAA46126 and AAB02825 to AAB02859 represent sequences used in the		
CC	exemplification of the present invention		
XX			
SQ	Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;		
	Query Match 58.4%; Score 686.6; DB 3; Length 1173;		
	Best Local Similarity 75.1%; Pred. No. 4e-204;		
	Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2		
QY	1 ATGTCGAGTCTACAGTACTGGGACATCTTGGCCACAGCTGCTCAGTCCCTTTGGCATTT 60		
Db	1 ATGCCAGATACTAATAGCACAACTCAATCAATTTATCATAAGCACTCGTGTACTTTAGCATTT 60		
QY	61 TTAATGCTTCATTTGGCTTTGCTTATATAGTGTAGGCAATGCTGTGTCATCTTAGCCCTTT 120		
Db	61 TTTATGTCCTTAGTAGCTTTTGGCTATAATAGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120		
QY	121 GTGTGGACAGAAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180		
Db	121 GTGTGGACAAAAACCTTAGACATCGAAGTAGTATTTTTTCTTAATCTTGCCATCTCT 180		
QY	181 GACTTCCTCGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTTTAACATGG 240		
Db	181 GACTTCTTTTGGGTGTGATCTCCATTCCTTTGTATACCTCTCACACGCTGTTCCAAATGG 240		

Qy	241	AATTTTGGAAAGTGGAAATCTGATGATGTTTTGGCTCAATTA	CTGACTGATCTTTTGTGCAACCGCA	300
Db	241	GAATTTTGGAAAGGAAATCTGTGTAATTTTGGCTCACTGA	CTGACTGATCTGTATGTATGACACA	300
Qy	301	TCCTGCTACAAATAATGTTCCTCATTTAGCTACGATCGAT	ACGATACGATGTTTCAAAATGCTGTG	360
Db	301	TCTGTATATAACATATGTCTCTCAT	CAGCTATGATCGATACCTGTGAGTCTCAAAATGCTGTG	360
Qy	361	TCATTATAGGGCTCAACACACACTGGGCATCATGAAGAT	TGTTGCTCAAAATGGTGGCTGTTTGG	420
Db	361	TCATTATAGAACTCAACACTACTGGGGCTCTTGAAGAT	TGTTACTCTGATGCTGGCCGGTTTGG	420
Qy	421	ATACTGGCTTTCCTTGGTAAATGGCCCGATGATTCCTG	CGCTTCAGATTCCTTGGAAAGACAGC	480
Db	421	GTGCTGGCCCTTCTTAGTGAATGGCCCAATGATTCCT	AGTTCCTTTCAGAGTCTTGGGAAGGA----	476
Qy	481	ACGAACACAAAGGACTGTGAGCCTGGCTTCTGTTACAG	ATGCTGATACCTCCACCAATTACA	540
Db	477	--TGAAAGGTAGTGAATGTGAACCTGGGATTTTTTTC	CGGAATGGTATACATCCTTGGCCATCACA	534
Qy	541	ATGCTCTTTGGAATTTCCCTGCTTCCTGTCATCTCTG	CTGGCTTATTTCAATGTACAGATTTTAC	600
Db	535	TCATTTCTTGGNAATTCGTGATCCCACTCATCTT	AGTTCGCTTATTTCAATGAATATTTAT	594
Qy	601	TGGAGCCTGTGGAAAGCTAGGGCTCTCAGTAGTGGCC	CTACCCATGCTGGATTCCTCCACT	660
Db	595	TGGAGCCTGTGGAAAGCGTGTATCTCAGTAGTGGCC	AAAGCCATCCTGGAGTGACTGCT	654
Qy	661	ACCTCTTCCAGTGCTTCAGGACACTTACAGAGCTGG	GGTGGCTTCGACAGACAGTAAT	720
Db	655	GTCTCTTCCCAACATCTGTGGACACTCAATTCAG	AGGTAGACTATCTTCAAGGAGATCTCTT	714
Qy	721	CCTGGATTTGAAGGAATCAGTGTGCATCTCGTCACT	CAGAAAAGTCTCTCGAAGAAAGAGCAGC	780
Db	715	TCCTGATCGACAGAAGTTCTCTGCATCCTTTCATT	CAGAGACACAGAGGAAGAAGTAGT	774
Qy	781	ATCCTGTGTCTTTAAGGACTCATGAAACAGCAGTA	TCATCTGCTCTCAAAATGGGTGCC	840
Db	775	CTCATGTTTTCTCTCAAGAACCAAGATGAATAGCA	ATAAAATGCTTCCAAAATGGGTGCC	834
Qy	841	TTCTGGCGATTCGGAAGCTGACGCTTCGGCCAAAG	GGAGTACGACAGCTTCTCAGAGGC	900
Db	835	TTCTCCCAATCAGATTCCTGTAGTCTTTACCAAA	AGGGAAACATGTTGAATCTCTTAGAGCC	894
Qy	901	AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGT	AGCGCTTTTTCGCAATTTGCTGGGCTCCA	960
Db	895	AGGAGATTACCAAGTCACTGGCCATTTCTCTT	AGGGGTTTTTGTGTTTGTCTGGGCTCCA	954
Qy	961	TACTGTCTGTTTCAAAATGTGCTTTTCAACTTTA	CCCAAGACGGAAACGCCCAAAATCGGTG	1020
Db	955	TAATCTCTGTTTCAAAATGTGCTTTCAATTTAT	TTCTCTCAGCAACAGGTCCTTAAATCAGTT	1014
Qy	1021	TGGTACAGCATTCCTTCTGGCTGCAATGCTCAAT	TCGTTGTTTAAATCCCTTTCGTGAC	1080
Db	1015	TGSTATAGAATTCGATTTTGGCTTCAGTGGTTC	AAATTCCTTTGTCAATCTCTTTTGTAT	1074
Qy	1081	CCTTTGTGTCAAGGCGTTTCCAGAAAGCTTTCT	TGGAAAGATACATTTTGTGTGACAAAGCAA	1140
Db	1075	CCATTGTGTCAAGCGCTTTCAAAAGGCTTTCT	TGAAATATATTTTGTATATAAAAGCAA	1134
Qy	1141	CCAGCGCTGTCAAGAAC----	CAGTCACTATCTTCTTGA	1176
Db	1135	CCTCTACATCAAAACACAGTCCGTCACTATCTT	CTTAA	1173

RESULT 5	
AAD01124	
ID	AAD01124 standard; cDNA; 1173 BP
XX	
AC	AAD01124;
XX	
DT	02-NOV-2000 (first entry)

XX Human orphan G protein-coupled receptor hrUP7 cDNA.
DE
XX
XX Human, orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;
KW transmembrane receptor; signal cascade; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS l..1173
FT /*tag= a
FT /product= "hrUP7"
FT /note= "Human orphan G protein-coupled receptor."
XX
XX WO200031258-A2.
XX
XX 02-JUN-2000.
XX
XX 13-OCT-1999; 99WO-US023687.
XX
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123949P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 29-JUN-1999; 99US-0141488P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156633P.
XX 29-SEP-1999; 99US-0156634P.
XX 29-SEP-1999; 99US-0156653P.
XX 01-OCT-1999; 99US-0157280P.
XX 01-OCT-1999; 99US-0157281P.
XX 01-OCT-1999; 99US-0157282P.
XX 01-OCT-1999; 99US-0157293P.
XX 01-OCT-1999; 99US-0157294P.
XX 12-OCT-1999; 99US-00416760.
XX 12-OCT-1999; 99US-00417044.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX
XX Chen R, Dang HT, Liaw CW, Lin I;
XX
XX WPI; 2000-400068/34.
XX P-PSDB; AAY71297.
XX
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs for
PT use in the identification of G protein-coupled receptor agonists.
PT
XX
XX Claim 25; Page 59; 102pp; English.
XX
XX The present sequence is a cDNA encoding hrUP7, an endogenous human orphan
CC G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned
CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
CC GPCR of the invention, like all GPCRs has seven transmembrane alpha
CC helices with an extracellular N-terminus and an intracellular C-terminus.
CC However, no endogenous ligands has yet been identified for the proteins
CC of the invention. The orphan GPCRs may be used in the identification of
CC their endogenous ligands, and to screen potential GPCR agonists and
CC antagonists for use as pharmaceutical agents. The proteins may also be
CC used in the study of GPCR-mediated signalling cascades, and to elucidate
CC their precise role in normal and diseased human conditions. Nucleic acid
CC encoding human orphan GPCRs may be used for tissue localisation
CC expression analysis to provide information about their function in
CC healthy and pathological states
XX
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Qy 1 ATGTGGAGTCTAACAGTACTTGGCACTTTCGCCACCAGCTCTCTCAGGTCCCTTGGCAATTT 60
Db 1 ATGCCAGATCTAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGCTCTCAATTGGCTTTGCTATAATGGTAGGCAATCTGTGGTCACTTTAGCCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCACTTTTAGCTTTT 120
Qy 121 GTGGTGACAGAAAACCTTAGACATCGAAGTAATTTATTTTTTCTTAATTTGGCTATTCT 180
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCCTCGTGGTTTGTATTCCTCTGTATCATCCCTCAGTCTCAGTGTGTGTTTAATCGG 240
Db 181 GACTTCCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGCGCTGTTCGAATGG 240
Qy 241 AATTTGGAAAGTGGAAATCTGCATGTTTTGGCTCAATTAATGCTATCTTTTGTGCACCGCA 300
Db 241 GATTTTGGAAAGAAATCTGTGTAATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy 301 TCTGTCTACAATATTTGTCTCTTATAGCTACGATCGATACCAAGTCAGTTTCAAAATGCTGTG 360
Db 301 TCTGTATATAACATTTGTCTCTCATCAGCTATGATCGATACCTGTTCAGTCTCAAAATGCTGTG 360
Qy 361 TCTTATAGGCTCAACACACATCGGATCATGAAGATTTGCTCAATTTGGTGGCTGTTTGG 420
Db 361 TCTTATAGAACTCAACACATCTGGGGCTTTGAAGATTTGTTACTCTCTGATGGTGGCGCTTTGG 420
Qy 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGAAGAACAGC 480
Db 421 GTGCTGGCTTTCTTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGAAGAAGA --- 476
Qy 481 ACGAAACAAAGGACTGTGAGCCTGGCTTTGTATACAGAGTGGTACATCTCCACATTTACA 540
Db 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATACATCTTCCATCACA 534
Qy 541 ATGCTCTTGGAAATTCCTGTCTCTGTGATCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Db 535 TCATTTCTTGAATTCGTGATCCAGTCACTCTTAGTCTGCTTTATTTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGTGGCTTAGCCATGCTGGATTTCTCCACT 660
Db 595 TGGAGCCTGTGGAAGCGTGAATCTCAGTAGTGGCCAAAGCCATCTCGACTGACTGCT 654
Qy 661 ACCTCTTCCAGTGTCTTCCAGGACACTTACACAGAGCTGGGGTGGCTTCAGGACAAAGTAAT 720
Db 655 GTCTCTTCCAACTCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CTTGGATGAAGGAATCAGCTGCAATCTCGTCACTCAGAAAAGTCTCTGAAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAAAGTTCTCTGCATCTCTTCAATTCAGAGAGACAGAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTGCTTAAAGACTCAATGAACAGAGATATCACTGCTTTCAAAGTGGTTC 840
Db 775 CTATGTTTTTCCCTCAAGAAACAAGATGAATAGCAATACAATTTGCTTCCAATATGGTTC 834
Qy 841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTAGTCAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTTTCCAAAGGGACATGTTGAATGCTTTAGAGCC 894
Qy 901 AGGAAGCTAGCAGGTCACTGGCCATCTCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTCAAATTTGCTTTCACTTACCTCCAGAGCGGAACGCCCAATCGGTG 1020
Db 955 TATTCTCTGTTCACAAATTTGCTTTCAATTTATTTCTCAGCAACAGGTCTCTAAATCAGTT 1014
Qy 1021 TGGTACAGCATTTGCTTCTGGCTGCAATGGTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080

Db 1015 TGGTATAGATTGCAATTTGGCTTCAGTGGTTCAATTCCTTTGTCATCTCTTTTGAT 1074
Qy 1081 CCTTTGTCACAGCGCTTCCAGAGGCTTCTCGAAGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTACAGCGCTTCCAAAGGCTTCTTGAAATATATTTGTATATAAAAGCAA 1134
Qy 1141 CCAGCGTGTACAGAAC--CAGTCAGTATCTCTTGA 1176
Db 1135 CCTCTACATCAACAACAGTCGGTCAGTATCTCTTAA 1173

RESULT 6

AAF83203

ID AAF83203 standard; cDNA; 1173 BP.

AC

AAAF83203;

XX

DT 09-JUL-2001 (first entry)

XX

XX Human GPCR-like polypeptide, PFI-013 encoding cDNA.

XX

G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;
antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
osteopathic; neuroprotective; nootropic; dermatological; gynecological;
signal transduction; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

CDS 1..1173

FT /*tag= a

FT /product= "PFI-013"

XX

PN EP1096009-A1.

XX

XX 02-MAY-2001.

XX

XX 24-OCT-2000; 2000EP-00309364.

XX

XX 29-OCT-1999; 99GB-00025641.

XX

XX 20-APR-2000; 2000GB-00009973.

XX

XX (PFI2) PFIZER LTD.

XX

XX (PFI2) PFIZER INC.

XX

XX Peter B. O'reilly MA;

XX

XX WPI; 2001-309854/33.

XX

XX P-PSDB; AAB62445.

XX

XX New G-protein coupled receptor-like polypeptide, polynucleotide for

XX

XX screening drug candidates for treating diseases associated with signal

XX

XX transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.

XX

XX Claim 1; Page 43; 66pp; English.

XX

This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor
(GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
expressed by standard recombinant methodology. Antibodies and modulators
of PFI-013 are useful in the manufacture of a medicament for treating
allergic disorder, including extrinsic asthma, immunological disorders,
such as intrinsic asthma, vasculitic granulomatous disease, interstitial
and other pulmonary disease, including chronic obstructive pulmonary
disease (COPD), infectious, inflammatory disease, such as inflammatory
bowel disease and neoplastic and myeloproliferative diseases. They are
also useful for treating obesity, diabetes, metabolic, neurological
diseases, psychotherapeutics, urogenital disease, reproduction and sexual
medicine, inflammation, cancer, tissue repair, dermatology, photogeing,
skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
diseases, allergy and respiratory disease, sensory organ disorders, sleep
disorders and hair loss. The PFI-013 protein and nucleic acid are useful
in the diagnosis and treatment of the above conditions and also for

CC

CC screening drug candidates for the treatment of diseases associated with
CC signal transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples

XX

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match

Best Local Similarity 58.4%; Score 686.6; DB 4; Length 1173;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATTT 60

Db 1 ATGCCAGATACATAAGCACAAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

Qy 61 TTAATGTCCTTCAATTTGGCTTTGTATTAATGGTAGGCAATGCTGTGGTCATCTTACGCTTTT 120

Db 61 TTTATGTCCTTAGTAGCTTTTGGCTATTAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120

Qy 121 GTGGTGACAGAAACCTTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCT 180

Db 121 GTGGTGACAGAAACCTTTAGACATCGAAGTAGTATTTTCTTAATTTGGCTATTTCT 180

Qy 181 GACTTCCCTCGTGGTGTGATTTCCATTTCCCTGTACATCCCTCAGGTGTTGTTAACTGG 240

Db 181 GACTTCTTTGGGTGTGATCTCCATTTCTTTGTACATCCCTCAGCGTGTTCGAATGG 240

Qy 241 AATTTTGGAAAGTGGAAATCTGCATGTTTTGGTCTCAATTAATGCTATCTTTTGTGACCGCA 300

Db 241 GAATTTGGAAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300

Qy 301 TCTGTCTACAAATATTTGCTCATTAGCTAGCTAGTACGATACCACTCAGTTCAAATGCTGTG 360

Db 301 TCTGTATATAACATTTGCTCATCAGCTAGTATGATGATGATGATGATGATGATGATGATG 360

Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTTTG 420

Db 361 TCTTATAGAACTCAACATCTGSGGCTTGAAGATTGTTACTCTGATGGTGGCCGTTTG 420

Qy 421 ATACTGCTTTCTTTGGTAAATGGCCGATGATTTCTGGCTTTCAGATTTCTTGAAGAAGCAGC 480

Db 421 GTGCTGCGCTTCTTTAGTGAATGGCCCAATGATTTCTAGTTTTCAGAGTCTTGAAGGA--- 476

Qy 481 ACGAAACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCCACCATTACA 540

Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTCCCATCACA 534

Qy 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600

Db 535 TCATTTCTTGAATTCGTGATCCCAAGTCACTTATGTCGCTTATTTTCAACATGAATATTAT 594

Qy 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCGCTTAGCCATGCTGGATTTCCACT 660

Db 595 TGGAGCTGTGGAAGCGTAGATCTCAGTAGGTGCGCAAGCCATCTCTGGACTGACTGCT 654

Qy 661 ACCTTCTCAGTCTTCAGGACACTTACAGAGCTGGGGTGGCTTCAGGACAAAGTAAT 720

Db 655 GTCTCTTCCAACTCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714

Qy 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCCGAAAGAAAGCAGC 780

Db 715 TCTGCATCGACAAAGTTCTGCTATCTTCAATTCAGAGACACAGAGAGAAAGATAGT 774

Qy 781 ATCTGCTGCTCTTAAGGACTCAATGAACAGCAGTATCACTGCTTCAAAAGTGGTTC 840

Db 775 CTCTATGTTTCTTCAAGAACCAAGATGATAGCAATACATTTGTTCCAAAATGGTTC 834

Qy 841 TTTCTGGGATCGGAAAGTGTGAGCGCTTCGCAAGAGGAGTACGAGAGCTTCTCAGAGGC 900

Db 835 TTTCTCCCAATCAGATTTCTGTAGTCTTTCACCAAGGGAACATGTTGAATCTGTAGGCC 894

Qy 901 AGGAAGCTAGCAGGTCACTGCGCATCTTCTGAGCGCTTTTGCATTTTCTGGCTCCA 960

CC

Db 895 AGGAGATTACCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGGGCTCCA 954
QY 961 TACTGTCTGTTCACATGTCCTTTCACTTACCCAGACGGACGCCCAATCGGTG 1020
Db 955 TATTCTCTGTTCACATGTCCTTTCACTTACCCAGACGGACGCCCAATCGATT 1014
QY 1021 TGGTACAGCATGCTCTCGGCTGCAATGCTCAATTCGTTTGTATTCCTTCTGTAC 1080
Db 1015 TGGTATAGATTCGATTTTGGCTTCAGTGGTCAATTCCTTTGTCATCCTCTTTGTAT 1074
QY 1081 CCTTTGTTCACAGCGGTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTGGTTCACAGCGCTTTCAAAGGCTTTCTGAAATATTTTGTATATAAAGCAA 1134
QY 1141 CCAGCGCTTCACAGAAC---CAGTCAGTATCTCTTGA 1176
Db 1135 CCTCTACCATCAACAACAGTCGGTCAGTATCTCTTAA 1173

RESULT 7
AAH24007
ID AAH24007 standard; cDNA; 1173 BP.
XX
AC AAH24007;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human G protein-coupled receptor AXOR35 cDNA.
XX
KW AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; bipolar disorder; depression; delirium; dementia;
KW severe mental retardation; dyskinesia; Parkinson's disease;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery;
ss.
XX
OS Homo sapiens.

Key Location/Qualifiers
CDS 1..1173
/*tag= a
/product= "Human AXOR35"
/note= "G protein-coupled receptor"
XX
WO200133221-A1.
XX
PN 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;
XX Michalovich D, Morrow DM, Zhu Y;
XX WFI; 2001-316464/33.
XX P-PSDB; AAB73622.
XX
XX Novel G-protein coupled receptor polypeptide and polynucleotide for
XX treating cancer, autoimmune, pulmonary, cardiovascular and neurological
XX disorders and for identifying modulators useful for treating asthma.
PT

XX
PS
XX
CC The invention relates to the human G protein-coupled receptor AXOR35
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC transmembrane domains and is involved in signal transduction. AXOR35 has
CC homology and structural similarity with G protein-coupled receptors such
CC as the human histamine H3 receptor. The invention also relates to
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
CC and nucleotides may be used to treat a wide variety of disorders
CC including bacterial, fungal, protozoal and viral infections, particularly
CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
CC urinary retention; acute heart failure; hypotension; hypertension; angina
CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
CC psychotic and neurological disorders such as anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia, and severe mental
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
CC antibodies may be used in screening compounds for their ability to
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are
CC particularly useful for treating asthma, and inhibiting or promoting the
CC function of lymphocytes, macrophages, eosinophils or neutrophils in
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
CC useful for diagnosing or determining susceptibility of an individual to a
CC disease via the detection of abnormal levels of protein or mRNA, or via
CC the detection of mutations in the corresponding gene. AXOR35 proteins are
CC also useful for inducing an immunological response in a mammal against
CC the above diseases, and for antibody production. AXOR35 nucleotides are
CC also useful as diagnostic reagents, in chromosome localisation and tissue
CC expression studies, and for producing transgenic animals useful in drug
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
CC protein or fragments thereof, and are also useful for treating conditions
CC associated with the expression of the AXOR35 protein. The present
CC sequence represents cDNA encoding human AXOR35
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 5; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
QY 1 ATGTCGAGTCTAACAGTACTGCGCATCTGCCACCAGCTGCTCAGGTCCCTTGGCATTT 60
Db 1 ATGCCAGATACTAATAGCACAAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGTCCTTTCATTGTCCTTTGCTATAATGTTAGGCAATGCTGGTGCATCTTAGCCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAAAGCTAGGAATGCTTTGGTCACTTTAGCTTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 180
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTTGGCCATCTCT 180
QY 181 GACTTCCTCGTGGGTTTGATTTCATTCCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
Db 181 GACTTCCTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCAGCTGTTTGGAAATGG 240
QY 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
QY 301 TCTGTCTACAAATATTTGTCCTCATTAGCTAGCATCGATACCCAGTCAGTTTCAAAATGCTGT 360
Db 301 TCTGTATATAACATTTGTCCTCATTAGCTAGCATCGATACCCAGTCAGTCTCAAAATGCTGT 360
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGCTGCTTTGG 420
Db 361 TCTTATAGAACTCAACACTGCGGGCTTTGAAGATTGTTTACTCTGATGTTGGCCGTTGG 420


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QY 421 ATACTGGCTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGAGAACAGC 480
Db 421 GTGTGGCTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTTCTTGGAGAACAGC 476
QY 481 ACAGAACACAAAGGACTGTGAGCTGGCTTTGTACAGAGTGGTACATCTTCACCATTTACA 540
Db 477 --TGAAGGTAGTGAATGTAACCTGGATTTTTCGGAATGGTACATCTTCGCAATCACA 534
QY 541 ATGCTCTTGAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTTAC 600
Db 535 TCATTTCTTGAATTCCTGATCCAGTCACTTGTAGTGGCTTATTTCAACATGAATATTTAT 594
QY 601 TGGAGCTGTGGAGGCTAGGGCTCTCAGTAGTGGCTTCCAGCCATGCTGGATTTCTCCACT 660
Db 595 TGGAGCTGTGGAGGCTAGTATCTCAGTAGTGGCTTCCAGCCATGCTGGAGTGGCTGCT 654
QY 661 ACCTCTTCCAGTCTTCCAGACACTTACACAGAGCTGGGGTGGCTTCCAGGACAAAGTAAT 720
Db 655 GTCTCTTCCAACTCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CCTGGATTTGAAGGAATCAGTGTGATCTGTCATCTGTCAGAAAGTCTCTGAGAAAGAGCAGC 780
Db 715 TCTGCAATCAGAAAGTCTGTCATCTTCAATTCAGAGACACAGAGGAGAAAGAGTAGT 774
QY 781 ATCTGTGTCTTAAAGACTCAGTGAACAGCAGTATCACTGCTTCAAGTGGGTTC 840
Db 775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATCAATTTCTTCCAAATGGGTTC 834
QY 841 TTTCTGGCATCGAAAGTGCAGGCTTTCGCAAGGAGTACGACAGCTTCTCAGAGGC 900
Db 835 TTTCTCCATCAGATTTCTGTAGTCTTTCACCAAGGGAACATGTTGACTGTCTTAGGCC 894
QY 901 AGGAAGTACGCGAGTCACTGGCCATCTTCTCAGCGCTTTTCCCAFTTCTGGGTCCA 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTTCTTAGGGGTTTTGTGTTGCTGGGTCCA 954
QY 961 TACTGTCTGTCAATTTGCTTTTCACTTCCAGAGGAGTACGAGGAGGAGGAGGAGGAGG 1020
Db 955 TATTTCTGTGTCAATTTGCTTTTCACTTCCAGAGGAGTACGAGGAGGAGGAGGAGGAG 1014
QY 1021 TGGTACAGATTCGCTTCTGGCTGCAATGGTTCATTTGTTTAACTTCTTCTGTAC 1080
Db 1015 TGGTATGAAATTCATTTTGGCTTCAGTGGTTCATTTCTTCTTCTTCTTCTTGTAT 1074
QY 1081 CTTTGTGTACAGGCTTTCCAGAGGCTTTCTGGAAGATCTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTACAGGCTTTCCAGAGGCTTTCTGAAAGGCTTTCTGAAATATTTTGTATAAAGCAA 1134
QY 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CTTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 8
ID ABZ80663
XX
AC
ABZ80663;
XX
DT 13-JUN-2003 (first entry)
DE Human histamine receptor coding sequence.
XX
KW human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
KW anti-migraine; cardiant; anti-rheumatic; anti-arthritis; antipsoriatic;
KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
XX psoriasis; receptor.
OS Homo sapiens.
XX
```

```
PH Key Location/Qualifiers
FT CDS 1..1173
FT /*tag= a
FT /product= "Histamine receptor"
XX
XX US6204017-B1.
XX
XX 20-MAR-2001.
XX
XX 07-OCT-1999; 99US-00414010.
XX
XX 07-OCT-1999; 99US-00414010.
XX (SCHE ) SCHERING CORP.
XX Behan JX, Hedrick JA, Laz TM, Monsma FU, Morse KL, Umland SP;
XX Wang S;
XX WPI; 2002-442063/47.
XX P-PSDB; ABO98629.
XX
XX New nucleic acid encoding antigenic part of human histamine receptor,
XX useful for preparing antibodies, e.g. for treating-histamine related
XX disorders.
XX
XX Example 1; Col 27-28; 19pp; English.
XX
XX This sequence represents the open reading frame for a human histamine
XX receptor (HR) designated SP9144. The sequence was isolated by searching
XX databases with the sequence of known G-coupled protein receptor (GPCR).
XX The gene is used for recombinant production of HR and for preparing
XX antibodies (Ab). These Ab are used to purify HR by immunoaffinity
XX chromatography, in immunoassay of histamine receptor, to identify cDNA
XX clones that express the receptor, as antagonist to block binding of
XX histamine (for treating any histamine-associated disorder) and to
XX generate anti-idiotypic antibodies. Agonists and antagonists of the HR
XX protein can be used in the treatment of e.g. inflammation, asthma,
XX allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
XX chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
XX sclerosis, inflammatory bowel disease and psoriasis
XX
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGGCCACGAGTCTCAGGTCCCTTGGCATTT 60
Db 1 ATGCCAGATCTAATAGCAATCAATTTATCTAAGCACTCGTGTACTTAGCATTT 60
QY 61 TTAATGTCTTCAFTTGGCTTTGCTATAATAGTGGCAATGCTGTGTCATCTTAGCCCTT 120
Db 61 TTTATGTCTTAGTAGCTTTTGGCTATAATAGTGGCAATGCTTTGGTCAITTTAGCTTTT 120
QY 121 GTGGTGCAGAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGGTGCAGAGAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTTGGCCATCTCT 180
QY 181 GACTTCTCGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGCTGTTGTTAACTGG 240
Db 181 GACTTCTTGTGGGTGTGATCTCCATTTCTGTATCCCTCACAGCTGTTGCGAATGG 240
QY 241 AATTTTGGAGTGGAAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCGCCGA 300
Db 241 GATTTTGGAGAAAGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
QY 301 TCTGTCTACAATATTCCTCATTAGTACGATACGATACAGTCAGTTCAAAATGCTGTG 360
Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATACGATACCTGTCAAGTCTCAAAATGCTGTG 360
QY 361 TCTTATAGGCTCAACACACTGGCATCAAGATTTGTTGCTCAAAATGGTGGCTTTGG 420
```

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Db 361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGTAGTGGCGCTTTGG 420
QY 421 ATACTGGCTTCTTGTGTAATGCGCCGATGATTTCTGGCTTCAGATTTCTTGGAGAACAGC 480
Db 421 GTGCTGGCCCTTCTTAGTAATGGCCAAATGATTCTAGTTTTCAGAGTCTTGGAAAGGA--- 476
QY 481 ACGAAACAAAGAGCTGTGAGCCTTGTGTTTACAGAGTGGTACATCTCTCCATTTACA 540
Db 477 --TGAAGTAGTGAATGTGAACTGGATTTTTCGGAATGGTACATCTCTGCCATCACA 534
QY 541 ATGCTCTTGAATTCCTGCTTCTCTGTCATCTCTGTGGCTTATTTCAATGACAGATTTAC 600
Db 535 TCATTCTTGAATTCGTGATCCCGAGTCATCTTAGTGGCTTATTTCAACATGAATATTTAT 594
QY 601 TGGAGCTGTGGAGCGTAGGGCTCTCAGTAGTGGCCCTAGCCATGCTGATTTCTCCACT 660
Db 595 TGGAGCGTGTGGAGCGTAGATCATCTCAGTAGTGGCCAAAGCCATCTCTGGACGTGCT 654
QY 661 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTTCGAGGACAAAGTAAT 720
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CTTGATTAAGGAATCAGCTGATCTGTCATCTCAGAAAGTCTCTCGAAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAGTCTCTGCATCTTTCATTCAGAGAGACAGAGGAGAAAGAGTAGT 774
QY 781 ATCTGGTGTCTTAAGGACTCATGACAGCAGTATCACTGCTTCAAGTGGGCTTCC 840
Db 775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATCAATTCCTTCCAAATATGGGTTC 834
QY 841 TCTGCGCATCGGAAAGTGCAGCGCTTTCGCCAAAGGAGTACGACAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCAACTCATCTGTAGCTCTTCCAAAGGGAACATGTTGAATGCTTAGAGCC 894
QY 901 AGGAAGTACGCCAGGTCACCTGCGCATCTTCTCAGCGCTTTTCCCATTTGCTGGGTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGTCCA 954
QY 961 TACTGTCTGTTCAAAATGTCCTTCACTTACCAGGAGGAAAGCCCAATCGGTG 1020
Db 955 TATTCCTGTGTCAAATGTCCTTCAATTTATTCCTCAGCAACAGGTCTCTAAATCAGTT 1014
QY 1021 TGGTACAGCAATCCCTTCTGGCTGCAATGTTCAATTCGTTGTTAATCCCTTCTGTAC 1080
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGTTCATTCCTTGTGCAATCTCTTTGTAT 1074
QY 1081 CTTTGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATATCTTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTACAGGCGTTTCAAAAGGCTTCTTGAATAATTTTGTATATAAAAGCAA 1134
QY 1141 CGAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTCTACCATCAACACAGTGGTCTGATATCTTCTTAA 1173
```

RESULT 9

ABQ78739

ID ABQ78739 standard; DNA; 1173 BP.

XX

AC

XX

DT 05-DEC-2002 (first entry)

DE

XX Nucleotide sequence of human histamine receptor.

KW Human; histamine receptor; receptor; inflammation; asthma; allergy;

KW atopic dermatitis; stroke; myocardial infection; migraine;

KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;

KW multiple sclerosis; inflammatory bowel disease; psoriasis;

KW intracellular second messenger pathway; cellular growth rate;

KW hormone secretion; gene; ss.

XX

OS Homo sapiens.

```
XX FH Key Location/Qualifiers
FT CDS 1..1173
FT /*tag= a
FT /product= "histamine receptor"
```

XX US2002098539-A1.

PN

XX

PD 25-JUL-2002.

XX

PF 19-MAR-2001; 2001US-00812216.

XX

PR 07-OCT-1999; 99US-00414010.

XX

PA (BEHA/) BEHAN J X.

PA (HEDR/) HEDRICK J A.

PA (LAZT/) LAZ T M.

PA (MONS/) MONSMA F J.

PA (MORS/) MORSE K L.

PA (UMLA/) UMLAND S P.

PA (WANG/) WANG S.

XX

PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;

PI Wang S;

XX

DR WPI; 2002-673827/72.

XX

DR P-PSDB; ABB78276.

XX

XX

PT Novel mammalian histamine receptor polypeptide useful for identifying

PT agonist or antagonist for treating diseases such as inflammation, asthma,

PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.

XX

PS Example 1; Page 15-16; 21pp; English.

XX

CC The present sequence encodes a human histamine receptor. The polypeptide

CC is useful for identifying an agonist or antagonist of a mammalian

CC histamine receptor. It is useful as an antigen to elicit the production

CC of antibodies. The histamine receptor polypeptide and polynucleotide are

CC useful in the treatment and management of diseases such as inflammation,

CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,

CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid

CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.

CC They are also useful for modulating intracellular second messenger

CC pathway activated through histamine receptors (cyclic-AMP, calcium,

CC inositol phosphate and mitogen activated protein (MAP) kinase), changes

CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+

CC mobilization, mitogenic effects, etc

XX

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4e-204; Indels 9; Gaps 2;

Matches 886; Conservative 0; Mismatches 284;

QY 1 ATGTCGGAGTCTAACAGTACTTGGCATCTTGCCACACAGCTGCTCAGGTCCCTTGGCATTT 60

Db 1 ATGCCAGATACATATAGACACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60

QY 61 TTAATGCTTTCATTTGCGCTTTGCTATATAAGTGGTCAATGCTGTGGTCACTTTAGCCTTT 120

Db 61 TTTATGCTCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCACTTTAGCTTTT 120

QY 121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTCTTCT 180

Db 121 GTGGTGGACAAAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCATCTCT 180

QY 181 GACTTCTCTGTTGGTGTGATTTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 240

Db 181 GACTTCTTGTGGTGTGATTCATTCCTTGTACATCCCTCACAGCTGTTTGAATGG 240

QY 241 AATTTTGGAAAGTGAATCTGCGATGTTTGGCTCAATCTACTGACTATCTTTTGTGACCGCA 300

Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300

```
QY 301 TCTCTACAAATATGTCCTCATTTAGCTACGATCAGTACCAGTCAGTTTCAAATGCTGTG 360
D 301 TCTGTATATAACAATGTGTCCTCATTCAGCTATGATCGATACCTGTCTCAGTCTCAAATGCTGTG 360
QY 361 TCTTATAGGGCTCAACACACTGGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG 420
D 361 TCTTATAGAACTCAACACTATGCGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
QY 421 ATACTGCTTCTTGGTAAATGGCCCGATGATTCGCTTCAGATTCTTGGAAAGAACAGC 480
D 421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATTCAGTTTTCAGAGTCTTGGNAGGA--- 476
QY 481 ACGNACAAAGGACTGTGACCTGGCTTGTGTTACAGAGTGGTACATCCTCACCATTACA 540
D 477 -TGAAGGTAGTGAATGGAACCTGGAATTTTTCGGAATGGTATACATCCTTGCCATCACA 534
QY 541 ATGCTCTTGAATTCCTGCTTCTCTGTCATCTCTGCTTATTTCAATGTACAGATTTCAC 600
D 535 TCATTCTTGGAAATTCGTGATCCCGAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
QY 601 TGGAGCTGTGGAAGCTAGGGCTCTCAGTAGGTGCGCTAGCCATGCTGGAATCTCCACT 660
D 595 TGGAGCTGTGGAAGCTGATCATCTCAGTAGGTGCGCAAGGCCATCTCGGACTGACTGCT 654
QY 661 ACCTCTTCCAGTGTCTCAGGACATTTACACAGAGCTGGGTGGCTTCGAGGACAGTAAT 720
D 655 GTCTCTTCTTCCAACTATCTGTGGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CCTGATTTGAAGGAATCAGCTGTCATCTCGTCACTCAGAAAGTCTCTCAAGAAAGAGCAGC 780
D 715 TCTGATCGACAGAAATGCTCTGCAATCTTCAATTCAGAGAGACAGAGGAAAGAGTAGT 774
QY 781 ATCTGCTGTCTTAAAGACTCACAAGACAGCAGTATCACTGCTTCAAAGTGGGTTC 840
D 775 CTCATGTTTCTTCCCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTC 834
QY 841 TCTGCGCATCGGAAATGAGCGCTTCGCGCAAGGAGTAGCAGAGCTTCTCAGAGGC 900
D 835 TTCTCCCAATCAGATTCTGTAGCTCTTTCAGCAAGGGAACATGTTGAATGCTTAGAGCC 894
QY 901 AGGAAGTACGAGTCACTGGCCATCTCTCTGAGCGCTTTTGGCATTTGCTGGGTCCA 960
D 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTGTGCTTTGCTGGGTCCA 954
QY 961 TACTGTCTGTTCAAAATGTCCTTTCAACTTACCCAGAGCGGAACGCCCAAAATCGGTG 1020
D 955 TATCTCTGTTCAAAATGTCCTTTCACTTTATTTATCTCTCAGCAACAGGTCTCTAATCAGTT 1014
QY 1021 TGGTACAGCAATGCTTCTGGCTGCAATGTTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080
D 1015 TGGTATAGAATTCATTTTGGCTTCAGTGGTTCATTTCAATTCCTTTGTCAATCCTCTTTTGTAT 1074
QY 1081 CCTTTGTGTACAGCGGTTTCCAGAGGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
D 1075 CCATTTGTGTACAGCGCTTTCAAAAGGCTTCTTGAANAATATTTTGTATATAAAGCAA 1134
QY 1141 CCAGCGCTGTACAGAAAC---CAGTCAGTATCTCTTGA 1176
D 1135 CCTTACCATCAACACAGTGGTCAAGTATCTCTTAA 1173
```

RESULT 10

AAI70980

ID AAI70980 standard; cDNA; 1173 BP.

XX AAI70980;

XX AAI70980;

XX 18-MAR-2002 (first entry)

XX Human histamine H4 receptor cDNA.

XX Histamine H4 receptor; human; antiasthmatic; antiallergenic;

KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;

XX diagnosis; gene therapy; ss.

OS Homo sapiens.

XX WO200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WPI; 2002-114339/15.

XX P-PSDB; AAM50564.

New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

Claim 4; Fig 1; 92pp; English.

The present sequence is that of cDNA clone pH4R encoding a human histamine receptor of the H4 subtype. The cDNA was isolated from a bone marrow cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 6; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

```
QY 1 ATGTGGAGTCTAACAGTACTGGGATCTTGGCACCAGCTGCTCAGGTCCCTTGGCATTT 60
D 1 ATGCCAGATATAATAGCACAAATCAATTTATCATTAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGTCCTTCAATTTGCTTTGCTATAATGTTAGGCAATGCTGGTGCATCTTAGCCCTT 120
D 61 TTTATGTCCTTAGTACTTTTGTCTATTAATGCTAGGAATGCTTTGGTCAATTTAGCTTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT 180
D 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTTTCTTAACCTTGGCCATCTCT 180
QY 181 GACTTCTCTGGGTGTTGATTCATTCCTCTGTACATCCCTCAGCTGTGTTTAACTGG 240
D 181 GACTTCTTGTGGGTGTGATCTCCATTTCTTTGTACATCCCTCAGCGCTTTCGAATGG 240
QY 241 AATTTTGGAGTGAATCTCATGTTTGGCTCATTAAGTACTGACTATCTTTTGTGCACGCA 300
D 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTATGACGCA 300
QY 301 TCTGTCTACAATATTTGTCCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAATGCTGTG 360
D 301 TCTGTATATAACATTTGTCCTCATCAGCTATGATCGATACCTGTCTCAGTCTCAAATGCTGTG 360
QY 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGTGTGG 420
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Db 361 TCTTATAGAACTCAACATCTGCGGCTCTGAAGATTGTTACTCTGATGTTGGCGCTTTGG 420
Qy 421 ATACTGCTTTCTTGGTAAATGGCCCAATGATTTCTGCGCTTCAGATTCTTGGAGAAACAGC 480
Db 421 GTGTGCGCTTCTTAGTGAATGGCCCAATGATTTCTAGTTTTCAGAGTCTTGGAAAGGA---- 476
Qy 481 ACGAACAACAAGAGCTGTGAGCCCTGGCTTTGTTTACAGAGTGGTACATCCCTCACCATTACA 540
Db 477 --TGAAGTGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCCTTGGCCATCACA 534
Qy 541 ATGCTCTTGGAAATTCCTGCTCTCTGTCATCTCTGTGCTTATTTCAATGTACAGATTTC 600
Db 535 TCATTCTTGGATTCGTGATCCCACTCATCTTAGTCTGTTATTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCCTAGGCTCTCAGTAGGTCCTTACGATGTCCTTCAAGTCTGCACT 660
Db 595 TGGAGCCTGTGGAAGCCTGATCATCTCAGTAGGTCCTTCAAGGCTTCAAGGCTGACTGCT 654
Qy 661 ACTCTTCCAGTCTTCAGACACTTACACAGAGCTGGGTGGCTTCGAGACAAAGTAAT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTGAAGAAATCAGCTGCTCATCTCGTCACTCAGAAAGTCTCCTGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAGTCTCTGCATCTCTTATTCAGAGACAGAGAGAGAGTAGT 774
Qy 781 ATCTGTGTCTTAAAGATCTACATGAACAGCAGTATCACTGCTTCAAGTGGGTTC 840
Db 775 CTATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834
Qy 841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAGGAGTACGACAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTGTAGTCTTTCACCAAGGGAACATGTTGAATGCTTAGAGCC 894
Qy 901 AGGAAGCTAGCAGGTCACCTGCGCATCTCTGAGCGCTTTTGCCATTGCTGGGCTCCA 960
Db 895 AGGAGATTGCCAAGTCACTGGCATCTCTTAGGGGTTTTTGTGTTGCTGGCTCCA 954
Qy 961 TACTGTCTGTCAAAATGTCCTTTCAACTTACCCAGAACGGAACGCCCAATCGGTG 1020
Db 955 TATTCTCTGTTCACAAATGTCCTTTCAATTTATTTCTCAGCAACAGGCTCCTAAATCAGTT 1014
Qy 1021 TGTACAGCATGCTCTCTGCTGCAATGTTCAATTCGTTGTTAATCCCTTCTCTGAC 1080
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTCAATTCCTTTGTCATCTCTTTGTAT 1074
Qy 1081 CCTTTGTGTACAGCGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGCACAAAGCAA 1140
Db 1075 CCATTGTGTACAGCGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134
Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACAAACAGTCGGTCAGTATCTTCTTAA 1173
```

RESULT 11

ACA93262
ID ACA93262 standard; cdna; 1173 BP.

XX ACA93262;

XX 16-JUL-2003 (first entry)

XX Human cdna encoding GPCR hrup7.

XX Human; ss: gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;
hARE-5; hrup3; hrup5; hrup6; hrup7; hGPCR27; hARE-1; hARE-2; hrup1; hG2A;
hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hruf4; signalling cascade.

XX Homo sapiens.

XX US2003017528-A1.

```
XX 23-JAN-2003.
XX 06-JUN-2001; 2001US-00875076.
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123949P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 28-JUN-1999; 99US-0141448P.
XX 28-SEP-1999; 99US-0156333P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156634P.
XX 12-OCT-1999; 99US-00417044.
```

(CHEN/) CHEN R.

(DANG/) DANG H T.

(LIAW/) LIAW C W.

(LINI/) LIN I.

Chen R, Dang HT, Liaw CW, Lin I;

WPI; 2003-428952/40.

P-PSDB; ABU92265.

Novel endogenous, orphan, human G protein-coupled receptors useful for
identification of modulators of the receptor and as research tools for
understanding the role of the receptor in human body.

Claim 25; Page 22; 54pp; English.

The invention relates to a human G protein-coupled receptor (GPCR)
appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named
hARE-3, hARE-4, hARE-5, hrup3, hrup5, hrup6, hrup7, hGPCR27, hARE-1, hARE
-2, hrup1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hruf4.
Also included are a plasmid comprising a vector and one of the cDNAs
above and a host cell comprising the plasmid. The GPCRs are useful for
the direct identification of candidate compounds as inverse agonists,
agonists or partial agonists. In vitro and in vivo systems incorporating
GPCRs is useful for elucidating and understanding the roles these
receptors play in the human condition, both normal and diseased, as well
as understanding the role of constitutive activation as it applies to
understanding the signalling cascade. The cDNAs are useful for making a
probe for dot-blot analysis against tissue mRNA and/or RT-PCR
identification of the expression of the receptor in tissue samples. The
present sequence is a cDNA encoding a GPCR of the invention

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 8; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4e-204;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCCTTGGCAATTT 60

Db 1 ATGCCAGTACTAATAGCACAAATCAATTATCACTAAGCACTCGTGTTACTTTAGCAATTT 60

Qy 61 TTAATGCTTCAATTTGCTTTGCTTATTAATGTTAGGCAATGCTGTGTCATCTTAGCCCTTT 120

Db 61 TTTATGCTCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120

Qy 121 GTGGTGACAGAAACCTTAGACATCGAATAATTTTTCCTTAATTTGCTGCTATTTCT 180

Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTTTTCTTAATCTGCGCATCTCT 180

Qy 181 GACTTCTCTGGGGTTTGTATTTCCATTCCTCTGTACATCCCTCACGTGTTCTTTAACTGG 240

CC vaccines, or for treating infections (bacterial, fungal, protozoan or
CC viral infections), transplant rejection, gastrointestinal disorders (such
CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
CC irritable bowel syndrome, vomiting, inflammation (such as atopic
CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
CC psoriasis), urological diseases (such as urinary retention),
CC cardiovascular diseases (such as myocardial infarction), hypotension,
CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary
CC disease), cough, renal diseases (such as renal ischaemia);
CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders
CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft
CC versus host disease and osteoporosis. The present sequence is the cDNA
CC encoding AXOR35
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 58.4%; Score 686.6; DB 10; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGGTCCTTGGCAATTT 60
Db 1 ATGCCAGATCTAATAGCACAACTCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 61 TTAATGTCCTTCAATTTGGCTTGTATTAATGGTAGGCAATGCTGTGGTCATCTTAGCCCTTT 120
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Qy 181 GACTTCCTCGTGGGTTTGAATTTCCATTCCTCTGTACATCCCTCACGCTGTTGTTAACTGG 240
Db 181 GACTTCCTTGTGGGTGTGATCTCAATCTCTTGTACATCCCTCACGCTGTTGCGAATGG 240
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Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTCCTCAATGCTGGCTGTTTGG 420
Db 361 TCTTATAGAACTCAACATCTGGGCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
Qy 421 ATACTGGCTTCTTGGTGAATGGCCGATGATCTGCTTCAAGTTCAGATCTTGGAAAGACAGC 480
Db 421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATCTAGTTCAGAGTCTTGGAAAGCA--- 476
Qy 481 ACAGACAAAGACGCTGAGCTGGCTGTTTGTACAGAGTGGTACATCTCCATCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCAATCACA 534
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Db 595 TGGAGCTGTGGAAAGCGTAGATCTCTCAGTAGGTGCTTACGCAATGCTGGAATGCTGCT 654
Qy 661 ACTCTTCCAGTCTTACAGACACTTACAGAGCTGGGTGGCTTGCAGGACAGATTAAT 720
Db 655 GTCTCTTCCAACTCTGTGGACACTTATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTGAAGGAATCAGCTGCTGCTGCTCCTCAGTCAAGAGTCTCTGAAAGAAAGACAGC 780
Db 715 TCTGCATCGACAGAAAGTTCTTGCATCTCTTCAATTCAGAGAGACAGAGGAAAGAGTAGT 774

Qy 781 ATCTGTGTCTTAAAGACTCAGATCAACAGCAGAGTATCACTGCTTCAAGTGGGTTC 840
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Qy 841 TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGAGTACGACAGAGCTTCTCAGAGGC 900
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Qy 901 AGGAAGCTAGCAGGTCACTGGCCATCTTCTGTAGCGCTTTTGGCAATTTGCTGGGCTCCA 960
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 961 TACTGTCTGTTCACAAATGTCCTTCAACTTACCCAGAGCGGACGCCCAAAATCGGTG 1020
Db 955 TATTTCTGTTCACAAATGTCCTTCAATTTTATTTCTCAGCAACAGGTCCTTAATCAATG 1014
Qy 1021 TGGTACAGCAATGCTTCTGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTGAC 1080
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Qy 1081 CCTTTGTGTACAGGCGTTTCCAGAAAGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
Db 1075 CCATTTGTGTACAGGCGTTTCCAAAGGCTTTCTTGAATAATATTTGTATATAAAAGCAA 1134
Qy 1141 CCAGCGCTGTACAGAAC---CAGTCAGTATCTCTTGA 1176
Db 1135 CCTTACCATCAACACAGTCGGTCAGTATCTCTTAA 1173

RESULT 14
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ID ADJ26922 standard; cDNA; 1173 BP.
XX AC ADJ26922;
XX AC (first entry)
DT 20-MAY-2004
XX Human endogenous orphan G-protein coupled receptor RUP7 cDNA.
DE Human; G protein-coupled receptor; GPCR; dot-blot analysis;
KW pharmaceutical agent; gene; ss.
XX Homo sapiens.
FH Key Location/Qualifiers
CDS 1..1173
FT /*tag= a
ET /product= "Human endogenous orphan GPCR protein"
XX
PN US2003175891-A1.
XX
PD 18-SEP-2003.
XX
PF 21-MAR-2003; 2003US-00393807.
XX
PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123949P.
PR 28-MAY-1999; 99US-0136436P.
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PR 28-MAY-1999; 99US-0137127P.
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PR 28-JUN-1999; 99US-0156333P.
PR 28-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
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PR 01-OCT-1999; 99US-0157280P.
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PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00411044.
PR 17-OCT-2002; 2002US-00272983.
XX
CHEN R.
PA (DANG/) DANG H T.
PA (LIAM/) LIAM C W.
PA (LINI/) LIN I.
XX
Chen R, Dang HT, Liaw CW, Lin I;
XX
WPI: 2003-898539/82.
DR P-PSDB; ADJ26923.
XX
New human G protein-coupled receptor and its coding cDNA, useful for
PT disease or disorder identification and/or selection, for screening of
PT candidate compounds useful as pharmaceutical agents, and in research
PT applications.
XX
Claim 25; SEQ ID NO 13; 53pp; English.
XX
The present invention relates to human endogenous orphan G protein-
CC coupled receptor (GPCR) proteins and polynucleotides encoding such
CC proteins. The cDNA sequence of the human G protein-coupled receptor
CC (GPCR) is useful in making a probe for dot-blot analysis against tissue-
CC mRNA and/or for RT-PCR identification of the expression of the receptor
CC in tissue samples. GPCR sequences of the invention may be used in
CC disease/disorder identification and/or selection, in screening of
CC candidate compounds for use as pharmaceutical agents and in research
CC settings. The present sequence is human endogenous orphan GPCR cDNA.
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 58.4%; Score 686.6; DB 11; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4e-204;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
QY 1 ATGTCGAGTCTAACAGTACTGGCATCTTCCACCAGCTGCTCAGTCCCTGGCATTTT 60
DB 1 ATGCCAGATCTAATAGCACAAATCAATTTATCATCAAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGCTTTCATTGCTTTCATTAATGCTAGGCAATGCTGGTCACTTAGCCCTT 120
DB 61 TTTATGCTTTCATTGCTTTCATTAATGCTAGGCAATGCTGGTCACTTAGCCCTT 120
QY 121 GTGCTGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180
DB 121 GTGCTGACAGAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 180
QY 181 GACTTCTCTGGGTTTGAATTTCAATTCCTCTGTACATCCCTCAGCTGTTTAACTGG 240
DB 181 GACTTCTCTGGGTTGATCTCAATTCCTTTGTACATCCCTCAGCTGTTTAACTGG 240
QY 241 AATTTTGGAGTGAATCTGCATCTTTGGTCAATTAAGTCAATCTTTTGTGACCGCA 300
DB 241 GAITTTTGGAAAGGAATCTGTGATTTTGGTCAATTAAGTCAATCTTTTGTGACCGCA 300
QY 301 TCTGTCTACAAATATTTGCTCATTAGCTACGATACGATACGATTTCAAAATGCTGTG 360
DB 301 TCTGTATATAACATTTGCTCATCAGCTATGATGATGATACCTGTGCTCAAAATGCTGTG 360
QY 361 TCTTATAGGGCTCAACACATCGGCATCATGAAGATTTGCTCAAAATGCTGTGTTGG 420
DB 361 TCTTATAGAACTCAACATCTAGGGGCTTGAAGATTTGCTCAAAATGCTGTGTTGG 420
QY 421 ATACTGCTTTCTTGGTAAATGGCCCATGATTTCTGCTTCAGATTTCTTGAAGAACAGC 480
DB 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGAAGGA---- 476
QY 481 ACGAACACAAAGGACTGTGAGCCCTGGCTTTGTTACAGAGTGGTACATCTCCTCACCAITACA 540
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DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTCGGAATGGTACATCTTGGCATCACA 534
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600
DB 535 TCATTTCTGGAATTCGTGATCCAGTCATCTTAGTGGCTTATTTCAACATGAATATTAT 594
QY 601 TGGAGCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTTCTCACT 660
DB 595 TGGAGCTGTGGAAGCGTAGATCATCTCAGTAGGTGCCCAAGCCATCTGAGCTGACTGCT 654
QY 661 ACCTCTTCAGTCTTCAGGACACTTACAGAGCTGGGGTGGCTTCAGGACAGAGTAAT 720
DB 655 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTGAAAGAAAGAGCAGC 780
DB 715 TCTGCAATGACAGAGTTCTGTCATCTTTCATTCAGAGACAGAGAGAGAGTAGT 774
QY 781 ATCTCTGTGTCTTAAAGGACTCATGAACAGCAGATATCATCGCTTCAAAGTGGGTTC 840
DB 775 CTCATGTTTTCTCAAGAACCAAGATGATAGCAATTAATTCCTCAGCAACAGGTCTTCAAAATGGGTTC 834
QY 841 TTTCTGGGATCGGAAAGTGCAGCGCTTCGCCAAAGGAGTACGAGAGCTTCTCAGAGGC 900
DB 835 TTTCTCCCAATCAGATTCGTAGCTCTTCAACAAAGGGAACATGTTGAATCTGTAGAGCC 894
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGGCTTTTGCATTTTCTGCTGGCTCCA 960
DB 895 AGGAGATTAGCCAGGTCACTGGCCATCTTCTTAGGGGTTTTTGTCTGTTGCTGGCTCCA 954
QY 961 TACTGTCTGTTCACAAATGTCTTCAACTTACCCAGAAACCGGAAACGCCCAATCGGTG 1020
DB 955 TATTCCTCTGTTCACAAATGTCTTCAATTTATTCCTCAGCAACAGGTCTTAAATCAGTT 1014
QY 1021 TGGTACAGCATTCGCTTCTGGCTGCAATGGTTCAATTCGTTTGTATTCCTTCTGTAC 1080
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DB 1135 CCTCTACCATCACACACACAGCTGCTCAGTATCTTTAA 1173
RESULT 15
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ID ADG86374 standard; cDNA; 1173 BP.
XX
AC ADG86374;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human endogenous orphan GPCR hrup7 cDNA.
XX
KW Human; ss; gene; endogenous orphan GPCR; G protein-coupled receptor;
KW transmembrane domain 6.
XX
OS Homo sapiens.
XX
PN US2003229216-A1.
XX
PD 11-DEC-2003.
XX
PF 16-APR-2003; 2003US-00417820.
XX
PR 13-OCT-1998; 98US-00170496.
PR 12-NOV-1998; 98US-0108029P.
PR 20-NOV-1998; 98US-0109213P.
PR 27-NOV-1998; 98US-0110060P.
PR 16-FEB-1999; 99US-0120416P.
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Search completed: May 22, 2006, 19:21:36
Job time : 761 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 19:24:55 ; Search time 6433 Seconds
(without alignments)
10222.468 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atctcgagctcaacagctac.....accagtcagatctcttctga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est3.*

3: gb_est4.*

4: gb_est5.*

5: gb_est6.*

6: gb_est7.*

7: gb_est8.*

8: gb_est9.*

9: gb_est10.*

10: gb_est11.*

11: gb_est12.*

12: gb_est13.*

13: gb_est14.*

14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	438.6	37.3	839	4 BX643713	BX643713 DKFZp781C
2	426.4	36.3	704	5 CF147821	CF147821 AGENCOURT
3	258	21.9	721	8 CO959034	CO959034 AGENCOURT
4	140.8	12.0	2625	6 AK140374	AK140374 Mus muscu
5	139	11.8	791	10 DW582260	DW582260 EST_ssal
6	135.8	11.5	672	4 CB556920	CB556920 AMGNNUC:U
7	133.8	11.4	732	5 CF147822	CF147822 AGENCOURT
8	130.2	11.1	728	10 DT257276	DT257276 JGI_CAAU8
9	129.2	11.0	558	9 DA308555	DA308555 DA308555
10	129.2	11.0	853	5 CD326085	CD326085 AGENCOURT
11	126.8	10.8	542	10 DW576242	DW576242 EST_ssal
12	115.6	9.8	684	12 CC481311	CC481311 CH240_309
13	114	9.7	574	9 DA306992	DA306992 DA306992
14	106	9.0	755	9 DA728518	DA728518 DA728518
15	101.2	8.6	687	10 DY313565	DY313565 AGENCOURT
16	100.2	8.5	647	10 DV880423	DV880423 LB02613.C
17	99	8.4	643	1 AL848045	AL848045 AL848045
18	99	8.4	824	9 CX422842	CX422842 JGI_XZG63
19	96.2	8.2	716	8 CN423054	CN423054 170004245

20	95.8	8.1	569	9 DA257272	DA257272
21	95.6	8.1	499	7 BF567596	BF567596 UI-R-800-
22	95	8.1	575	9 DA360011	DA360011 DA360011
23	88.6	7.5	1046	3 BQ950659	BQ950659 AGENCOURT
24	87.6	7.4	921	14 CNS03296	AL224547 Tetraodon
25	82	7.0	838	10 DV891040	DV891040 LB02719.C
26	80.6	6.9	700	8 CO138455	CO138455 EST833126
27	80.6	6.9	754	3 BU468854	BU468854 603373878
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29	80.2	6.8	258	7 AM654609	AM654609 104607 MA
30	78.8	6.7	410	3 BQ836551	BQ836551 rf47c11.Y
31	77.8	6.6	814	10 DT311294	DT311294 JGI_CAAK2
32	77.6	6.6	727	8 CR366545	CR366545 CR366545
33	75.8	6.5	553	10 DW582261	DW582261 EST_ssal
34	75.8	6.4	523	2 BU122942	BU122942 BJ122942
35	75.8	6.4	565	4 CB385348	CB385348 OSTF021G5
36	75.8	6.4	582	2 BJ108530	BJ108530 BJ108530
37	75.8	6.4	633	2 BJ763892	BJ763892 BJ763892
38	75.6	6.4	1136	6 BC019470	BC019470 Mus muscu
39	74.8	6.4	562	2 BU103964	BU103964 BJ103964
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41	74.2	6.3	697	3 BU446363	BU446363 603213444
42	74	6.3	781	8 CK240157	CK240157 NMA02778
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44	74	6.3	1946	6 AK156130	AK156130 Mus muscu
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ALIGNMENTS

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DEFINITION BX643713 839 bp mRNA linear EST 04-SEP-2003
DKFZp781C0629_r1.781 (synonym: hlcc4) Homo sapiens cDNA clone
BX643713
ACCESSION BX643713 GI:34478046
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 839)
AUTHORS Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
TITLE EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp781C0629) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

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Query Match      37.3%; Score 438.6; DB 4; Length 839;
Best Local Similarity 75.9%; Pred. No. 3.8e-118;
Matches 570; Conservative 0; Mismatches 174; Indels 7; Gaps 2;

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Qy 181 GACTTCCTCGTGGGTTTGATTTTCATTCCTCTCTGTACATCCCTCACGTTGTTTAACTGG 240
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Qy 241 AATTTTGGAGTGGAACTCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCAACGCA 300
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Qy 301 TCTGTCTACAAATATGTCCTCATTTAGCTACGATCGATACCAAGTCAGTTTCAAATGCTGTG 360
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Qy 481 ACGAACACAAGAGCTGTGACCTGGCTTTGTTACAGAGTGTATACCTCCACCATTTACA 540
Db --TGAAGGTAGTGAATGTGAACCTGGGATTTTTCGGAATGGTACATCTCTTGGCCATCACA 629
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Qy 661 ACCTCTTCCAGTGTCTCAGGACCTTACAGAGCTGGGGTGGCTTCGAGACAAAGTAAT 720
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Db TCTGCACTGACAGAAGTCTCTGCACTCTTTC 839

RESULT 2
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LOCUS
DEFINITION AGENCOURT_14740195 NIH_MGC_145 Homo sapiens cdna clone
IMAGE:6971900 5', mRNA sequence.
CF147821
ACCESSION CF147821.1 GI:33244089
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaps-i@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: b column: 07
High quality sequence stop: 685.

FEATURES
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1. 704
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/db_xref="taxon:9606"
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varies by clone; ORFs were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 36.3%; Score 426.4; DB 5; Length 704;
Best Local Similarity 77.0%; Pred. No. 1.5e-114;
Matches 547; Conservative 0; Mismatches 156; Indels 7; Gaps 2;

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Qy 63 AATGCTCTTCAATTTGCTTCTGCTATATGTTAGGCAATGCTGTGTCATCTTAGCTTTGT 122
Db 61 TATGTCCTTAGTAGCTTTTGTCTATATGCTAGGAATGCTTTGCTCAATTTAGCTTTGT 120
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DEFINITION AGENCOURT 30842625 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389774 5', mRNA sequence.
ACCESSION CO959034
VERSION    CO959034.1 GI:51323616
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   NITH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: gcapsb-remail.nih.gov
          Tissue Procurement: Guthrie cDNA Resource Center
          cDNA Library Preparation: Guthrie cDNA Resource Center
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: IRB18 row: a column: 04
          High quality sequence start: 2
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             /notes="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image/rearrayed_plates/IRBF.presv.dat
a. Note: This is a NIH_MGC Library."

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Best Local Similarity 78.4%; Pred. No. 1.4e-64;
Matches 309; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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AK140374      2625 bp mRNA linear HTC 21-SEP-2005
Mus musculus adult male cortex cDNA, RIKEN full-length enriched
library, clone:R530005H20 product:histamine receptor H 3, full
insert sequence.
ACCESSION    AK140374
VERSION      AK140374.1 GI:74150094
KEYWORDS     HTC; CAP trapper.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE
AUTHORS      Carninci, P. and Hayashizaki, Y.
TITLE        High-efficiency full-length cDNA cloning
JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
PUBMED       10349636
REFERENCE
AUTHORS      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE        Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
PUBMED       11042159
REFERENCE
AUTHORS      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kizumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE        RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL      Genome Res. 10 (11), 1757-1771 (2000)
PUBMED       11076861
REFERENCE
AUTHORS      Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakawa, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadohira, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,

```

Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohetsuki,S. and Hayashizaki,Y.

RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

FUNCTIONAL annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

5

REFERENCE

AUTHORS

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedziarski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavalan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakaguchi,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Inotani,K., Ishii,Y., Tioh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

FANTOM Consortium

ANALYSIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12468651

6

REFERENCE

AUTHORS

Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagioli,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashizaki,Y., Hensch,T.K., Hirokawa,N., Hill,D., Hummel,L., Iacono,M., Ikeo,K., Iwano,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollas,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakachi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G.,

Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiyama,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H., van Nimwegen,S., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Bruscia,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessey,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

FANTOM Consortium

THE transcriptional landscape of the mammalian genome

Science 309 (5740), 1559-1563 (2005)

16141072

7

REFERENCE

AUTHORS

Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

RIKEN Genome Exploration Research Group

ANTISENSE transcription in the mammalian transcriptome

Science 309 (5740), 1564-1566 (2005)

16141073

8 (bases 1 to 2625)

REFERENCE

AUTHORS

Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Inotani,K., Itoh,M., Kangawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES

source

Location/Qualifiers

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DW582260
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EST.
SOURCE
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ORGANISM
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1 (bases 1 to 791)
REFERENCE
Koop,B.F., Davidson,W.S. and cGRASP Consortium.
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
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JOURNAL
COMMENT
Unpublished (2006)
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.
Marra, Bioinformatics Centre for Biomedical Research, University
of Victoria Jong Leong, BF Koop.
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Plate: 575
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High quality sequence stop: 791.
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contributors: Robert Davlin (DFO, Vancouver, B.C.)"
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Matches 257; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

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Db 519 CTTGATCAGCTTCGACAGATTTATATCTGTCAACAAGCGGTAGCTACAGGTCTCAGAA 578

Qy 378 CACTGGCATCATGAAGATTGTGCTCAAATGGTGGCTGTTTGGATACTGGCTTTCTTGGT 437
Db 579 AGGTGTGACCGGGAGGCTGTCTTGAAGATGATGAGTGTGTGGCTGCTTCTTCTACT 638

Qy 438 AAATGGCCCGATGAT 452
Db 639 CTATGGCCGACGAT 653
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RESULT 6
CB556920
LOCUS
DEFINITION
CB556920
CB556920
CB556920.1 GI:29496320
CB556920
672 bp mRNA linear EST 02-APR-2003
AMGNNUC:URGP1-00001-D6-A urgp1 (14349) Rattus norvegicus cDNA clone
urgp1-00001-d6 5', mRNA sequence.
CB556920
CB556920.1 GI:29496320
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KEYWORDS
SOURCE  Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
JOURNAL   Sciurognathi; Muridae; Murinae; Rattus.
COMMENT   1 (bases 1 to 672)

AUTHORS  Angen EST Program.
TITLE     Angen Rat EST Program
JOURNAL   Unpublished (2003)
COMMENT   Contact: Dan Fitzpatrick
          Angen, Inc
          One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
          Tel: 805 447-4881
          Plate: 00001 row: d column: 6.

FEATURES
source   Location/Qualifiers
1..672
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="urp1-00001-d6"
/clone_lib="urp1 (14349)"
/notes="Vector: pSPORT1; Rat GPCR library rearrayed
internal pSPORT vector"

ORIGIN
Query Match      11.5%; Score 135.8; DB 4; Length 672;
Best Local Similarity 57.2%; Pred. No. 2.6e-28;
Matches 267; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

QY      3  GTCCGAGTCTAACAGTACTGGCATCTGGCCACAGCTGCTCAGTCCCTCCCTGGCATTTT 62
DB      178  GCGCGTGTGAGCGGGCGCGCGCTCTCGGTGCTGACCGCTGCTCGTGGCT 237
QY      63  AATGTCTTCAATTTGCCCTTGTCTATAATAGTGGCAATGCTGCTCATCTTAGCCTTTGT 122
DB      238  CATGGCGTCTCATCTGTGGCCACAGTACTGGGCAACGGCTGGTCTATGCTCGCTTGGT 297
QY      123  GGTGGACAGAACTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCTGA 182
DB      298  GCGGAGATTCAGGCTCGGCACCCAGAACAACTTCTTGTGCTCAACCTGCCATCTCCGA 357
QY      183  CTTCTCTGCGGTGTTGATTTCCATCTCTGTATACCTCCCTCAGTGTGTTTAAC---TG 239
DB      358  CTTCTCTGCGGTGCTCTGTGATCCCATTTGATGACCTATGCTGACCGCGGTG 417
QY      240  GAATTTTGGAGTGGAACTCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCAACGC 299
DB      418  GACCTTCGCGCGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACTACTGTGTGCTC 477
QY      300  ATCTGTCTACAATTTGTCTCTATTAGTACGATCGATACAGTCACTGTTTCAATGCTGT 359
DB      478  CTCGGTCTTCAACATCGTACTCATGCTATGACCTATGACCGATTCCTGTGACTCGAGCTGT 537
QY      360  GTCTTATAGGGCTCAACACCTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTTG 419
DB      538  CTCTACAGGGCCAGCAGGGGACACGACGCGCGCTTCGGAAGATGSCACTGTGTG 597
QY      420  GATCTAGGCTTTCTTGGTAAATGCCCGATGATTTCTGGCTTCAGATT 466
DB      598  GGTGCTGGCCTTCTGTGTATGGGCTGCCATCTGAGTTGGAGT 644

RESULT 7
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LOCUS     CF147822
DEFINITION AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone
IMAGE:6971899 5', mRNA sequence.
ACCESSION CF147822
VERSION    CF147822.1 GI:33244090
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL   Homnidae; Homo.
COMMENT   1 (bases 1 to 732)
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics / NIH
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: GPCR Consortium
          cDNA Library Preparation: GPCR Consortium
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          plate: IRBI02 row: b column: 06
          High quality sequence stop: 610.

FEATURES
source   Location/Qualifiers
1..732
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971899"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH MGC 145"
/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match      11.4%; Score 133.8; DB 5; Length 732;
Best Local Similarity 53.5%; Pred. No. 1.1e-27;
Matches 329; Conservative 0; Mismatches 277; Indels 9; Gaps 2;

QY      3  GTCCGAGTCTAACAGTACTGGCATCTTGCCACAGCTGCTCAGTCCCTCCCTGGCATTTT 62
DB      76  GCGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGCGTGTGCGCGCT 135
QY      63  AATGTCTCTCATTTGCTTTGTATATGTTAGGCAATGCTGTGTCATCTTAGCCTTTGT 122
DB      136  CATGGCGTCTCATCTGTGGCACGGTGTGGGCAACGGCTGTATGCTCGCTTCGT 195
QY      123  GGTGGACAGAACTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCTGA 182
DB      196  GCGCGACTCGAGCTCCGCAACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGA 255
QY      183  CTTCTCTGCGGTGTTGATTTCCATCTCTGTATACCTCCCTCAGCTGTG---TTTAACTG 239
DB      256  CTTCTCTGTCGCGCGCTTCTGCACTCCACTGTATGACCTAGCTGACAGCGCGCTG 315
QY      240  GAATTTTGGAGTGGAACTCTGCATGTTTGGCTCATTTACTGACTATCTTTGTGCAACGC 299
DB      316  GACCTTCGCGCGGGCTCTGCAAGCTGTGGCTAGTAGTACTACTGCTGTGCACTC 375
QY      300  ATCTGTCTACAATTTGTCTCTATTAGTACGATCGATACAGTCACTGTTTCAATGCTGT 359
DB      376  CTCCTGCTTCAACATCGTGTCTATCAGTACGACCGCTTCTCTGCTCAGCCGAGCGGT 435
QY      360  GTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTTG 419
DB      436  CTCATACCGGGCCAGCAGGGTGACACGCGCGCGGAGTGTGCGGAAGATGCTGTGGTGTG 495
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QY 420 GATACGCTTTCTTGGTAATGGCCGATGATCTCGCTTCAGA-----TTCTTGAA 473
 Db 496 GGTCTGGCTTCTCTGCTGACGACGAGCCATCTGAGTGGGAGTACCTGTCGGGGG 555
 QY 474 GAACAGCACGAACACAAAGGACTGTGAGCCCTGGCTTTGTTACAGAGTGGTACATCTTCAC 533
 Db 556 CAGTCCATCCCGAGGCCACTGCTATGCGAGTCTCTACAACTGGTACTTCTTCAT 615
 QY 534 CATTACAATGCTCTTGGAAATCTCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACA 593
 Db 616 CACGGCTTCCACACTGAGGTCTTTACGCCCTTCTCAGCGCTCACTTTCTTTAACTTCAC 675
 QY 594 GATTACTGAGCCT 608
 Db 676 CATCTACCTGAACAT 690

RESULT 8
 DT257276 728 bp mRNA linear EST 18-AUG-2005
 LOCUS JGI_CAAU8039.fwd CAAU Pimephales promelas brain 7-8 month adults,
 DEFINITION males and females pooled (L) Pimephales promelas cDNA clone
 CAAU8039 5', mRNA sequence.

ACCESSION DT257276.1 GI:73559225

VERSION EST.
 KEYWORDS Pimephales promelas
 SOURCE Pimephales promelas

ORGANISM Pimephales promelas
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Pimephales.

REFERENCE 1 (bases 1 to 728)

AUTHORS Richardson, P., Lucas, S., Rokhsar, D., Detter, J. C., Ng, D. C.,
 Brokstein, P. and Lindquist, E. A.
 TITLE DOE Joint Genome Institute Pimephales promelas EST project
 JOURNAL Unpublished (2005)

COMMENT Other_ESTs: JGI_CAAU8039.rev

Contact: Lindquist, E. A., Richardson, P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 5600

Fax: 925 296 5710

Email: cdna@jgi-psf.org

cDNA Library Preparation: DOE Joint Genome Institute:

http://www.jgi.doe.gov

DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone id and the direction of sequencing. The suffix '.fwd'
 indicates a forward sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.

Plate: CAAU 0081 row: n column: 18

High quality sequence stop: 706.

Location/Qualifiers

FEATURES

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1..728
 /organism="Pimephales promelas"
 /mol_type="mRNA"
 /db_xref="taxon:90988"
 /clone="CAAU8039"
 /tissue_type="brain"
 /clone_lib="CAAU Pimephales promelas brain 7-8 month
 adults, males and females pooled (L)"
 /notes="vector: pCMVsp6; The library was made from dt
 primed cDNA and cloned into Invitrogen vector pCMVsp6.
 Poly A RNA were primed with an oligo dt primer (5'-
 GACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3') ligated
 to a SalI adapter (5'- TCGACCCACGCGCC and 5'-
 CGACGCGTGG) and digested with NotI. cDNA was size
 selected using 1.1% agarose gel electrophoresis (L
 -0.5-1.2k, M -1.2-2.5k, H ->2.5k) then ligated into NotI
 and SalI digested pCMVsp6 vector. The work was done at
 DOE Joint Genome Institute."

ORIGIN

Query Match 11.1%; Score 130.2; DB 10; Length 728;
 Best Local Similarity 57.3%; Pred. No. 1.2e-26;
 Matches 256; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
 QY 21 TGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTTTAAATGCTTCAATTTGCTT 80
 Db 256 TGGCCAGTTTACTCCATCCACCTCAATATTCCTGACAGTTCTCATGACACTGCTGT 315
 QY 81 TGTATTAATGGTAGGCAATGCTGTGGTCACTCTTAGCCCTTTTGTGTGGACAGAAACCTTAG 140
 Db 316 CGCCACGGTTCTCGGGAACGCGCTTGTCAITTTAGCTTTTGTGTGGAGAAAAGTTTACG 375
 QY 141 ACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGACTTCTCTCGGGTTTGTAT 200
 Db 376 CACAAAGGCAACTTTTCTTTTAAATTTGGCCATAGCGGACTTTCTTGTGCGTGGTT 435
 QY 201 TTCATTCTCTGTACATCCC--TCACGTGTTGTTTAACTTGGAAATTTTGGAACTGGAAT 257
 Db 436 TTGCATCCCGTGTATATTCCTATGTCCTGACGGGTGAGTGGAGGCTGGGCAGAGTCT 495
 QY 258 CTGCATGTTTGGCTCAATTACTGACTATCTTTTGTGTGACCGCATCTGTCTACAATATTGT 317
 Db 496 GTGTAAACTGTGGCTGGTAGTGGATTACATGTTGTGCACTGCCTCAGTCTTCAACATCGT 555
 QY 318 CCTCATTTAGCTAGATCGATACCATCAGTCAGTTTCAAAATGCTGTGCTTATAGGGCTCAACA 377
 Db 556 GCTCATCAGTTTTCGACAGGTTTCAGTCCGTCACATAAAGCGGTGAGTTACCATGCCAAAA 615
 QY 378 CACTGGCATCATGAAGATTGTTGCTCAATGGTGGCTTTTGGATACCTGGCTTTCTTGGT 437
 Db 616 GGGATCACCAGAGAGGCTGTTTGAAGATGCTCTGTGTGGCTTCGAGGTTCTCTCT 675
 QY 438 AAATGGCCCCGATGATTCTTGGCTTTCAGA 464
 Db 676 TTAATGGTCCAGCGATTATCAGTTGGGA 702
 RESULT 9
 DA308555 BRHIP2 Homo sapiens cDNA clone BRHIP2025783 5', mRNA
 LOCUS DA308555
 DEFINITION sequence.
 ACCESSION DA308555
 VERSION DA308555.1 GI:78290625
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 558)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 TITLE Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 1634560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction;
 Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,
 Research Association for Biotechnology (RAB) and Biotechnology

Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

1 (bases 1 to 542)

REFERENCE
AUTHORS Koop,B.F., Davidson,W.S. and cGRASP Consortium.
TITLE Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
JOURNAL Unpublished (2006)
COMMENT Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.
Marra. Bioinformatics: Centre for Biomedical Research, University
of Victoria Jong Leong, BF Koop.
Insert Length: 542 Std Error: 0.00
Plate: 566
Seq primer: M13 Reverse
High quality sequence stop: 542.

FEATURES
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/organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clone="ssal_19b2_566_015_rev"
/tissue_type="mixed tissue"
/clone_lib="rgb2"
/notes="Organ: brain, kidney, spleen; Vector: pCMVspout6;
ssalrgb2 mixed tissue Salmo salar cDNA; Tissue
contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN

Query Match 10.8%; Score 126.8; DB 10; Length 542;
Best Local Similarity 56.5%; Pred. No. 1.1e-25;
Matches 280; Conservative 0; Mismatches 207; Indels 9; Gaps 2;

QY 133 AACCTTAGACATCAAGTAATATTTTCTTAAATTTGGCTATTTCTGACTTCTCTCGTG 192
DB 1 AGCCTACGAATCAAAGCAACTACTTCTCTCAACCTTGCATTTTCAGATTTCTTGT 60

QY 193 GGTTTGATTTCCATCTCTGTACATCCCTCAGTGTGTTAA---CTGGAATTTGGA 249
DB 61 GGTGCAATCTGTATCCCTGTATACATCCCTCAACCTTGACAGCGCTGGTGGG 120

QY 250 AGTGGAACTGCGATGTTTGGCTCATTAAGTACTATCTTTTGTGCACCGCATCTGTCTAC 309
DB 121 AGAGTCTCTGTAAAGCTGTGGCTCTCATGAGTACTTGTCTGCACTGGCTCTGTCTTC 180

QY 310 AATATTGTCTCATTAAGTACGATCGATACAGTCAGTTTCAAATGCTGTCTTATAGG 369
DB 181 AACATAGTCTCATCAGCTATGACCGGTTCTCTCCGTCACGAGCAGTGAAATATAGA 240

QY 370 GCTCAACACTGGCATCATGAAGATTTGCTCAAAATGTTGGCTTTTGATCTGGCT 429
DB 241 GCTCAGCGGAGCATGACCCACCATGCTGTGTGAAGATGGTGGCTGTGTGGCC 300

QY 430 TTCTTGTAATAGCCCGGATTTCT-----GCCTTCAGATTTCTGGAAGAACAGCAGC 483
DB 301 TTCTTCTCTATGGCCCTGGCAATTAATCTTGGAGCTGGTTGGGTAAAGCATCGTT 360

QY 484 AACACAAGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCTCCATTCACATTAATG 543
DB 361 CCTGCCGACAGTGTTCGCTGAGTTCTACTGCACCTGGTACTTCTTACTCAGTGGCT 420

QY 544 CTCTTGAATTCCTGCTTCTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTACTGG 603
DB 421 ACGTTTGAGTTCTTCAACCCCTTTATCTCTGTGACCTTCTTCAACCTGTGCATCTACCTG 480

QY 604 AGCTGTGGAAGCGTA 619
DB 481 AACATCCAGAGGAGGA 496

RESULT 12
CC481311
LOCUS
DEFINITION
genomic survey sequence.

CC481311 684 bp DNA linear GSS 16-JUN-2003
CH240_309C10.T7 CHORI-240 Bos taurus genomic clone CH240_309C10,
genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus (cattle)

CC481311 GI:31760574
Bos taurus (cattle)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS
1 (bases 1 to 684)
Holt,R., Cloutier,A., Lee,D., Girm,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH240_309C10.TABAC13P2
Contact: Rob Holt

TITLE

JOURNAL

COMMENT

The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.choi.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.

Plate: 309 row: C column: 10

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. 684
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_309C10"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pTABAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 9.8%; Score 115.6; DB 12; Length 684;
Best Local Similarity 70.6%; Pred. No. 2.6e-22;
Matches 154; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 150 TAATATTTTCTTAAATTTGGCTATTTCTGACTTCTCTCGTGGGTTGATTTCCATTCC 209
DB 260 TACGTGCTATATTGTTGTTAACTTTTTCGCCCATGCGAGTATGATCTCAATCC 319

QY 210 TCTGTACATCCCTCAGCTGTGTTTAAGTGAATTTTGAAGTGAATTCGATGTTTG 269
DB 320 TTTATTCAATCCCTCACAAGCTCTTCAACTGGAGTTTGAATAAATCAATTTGTGTTTG 379

QY 270 GCTCATTACTGACTATCTTTTGTGCACCGCATCTGTCTACAATATTTGCTCATTAGCTA 329
DB 380 GTCACACTACTGACTATCTTTTGTGACGATCTGTGTATACATCGTACTCATCAGCTT 439

QY 330 CGATCGATACCACTAGTTCAAATGCTGTGCTTATA 367
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 Db 440 TGATCGATATCACTAGTCTCCAATGCTGTAACTCAA 477

RESULT 13
 DA306992 574 bp mRNA linear EST 28-OCT-2005
 LOCUS DA306992 BRHIP2 Homo sapiens cDNA clone BRHIP203706 5', mRNA
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdn@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan): cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES
 Source Location/Qualifiers
 1..574
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="BRHIP203706"
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 /note="Vector: pME18SFL3"

ORIGIN
 Query Match 9.7%; Score 114; DB 9; Length 574;
 Best Local Similarity 55.1%; Pred. No. 7.3e-22;
 Matches 269; Conservative 0; Mismatches 210; Indels 9; Gaps 2;

QY 151 AATATTTTCTTAATTTGGCTATTTCGACTTCCTGCTGGTTTGATTCATTCCT 210
 Db 16 AACTTCTTCCTGCTCAACCTCGGCATCTCCGACTTCCTCGTCGGCGCTTCTGCATCCCA 75
 QY 211 CTGTACATCCCTCAGCTGTGTTTAAAC--TGGAAATTTTGGAGTGGAAATCTGCATGTTT 267
 Db 76 CTGTATGATACCTACGTGCTGACAGGCGCTGGACCTTCGGCCGGGCGCTCTGCAAGCTG 135
 QY 268 TGGCTCATTTACTGACTATCTTTTGTGACCGGCATCTGTCTTACAAATATGTCCTCATAGC 327
 Db 136 TGCTGTGTAGTGAGTACCTGCTGTGCACCTCCTCTGCTTCAACATCGTGTCTCATCAGC 195
 QY 328 TAGCATCGATACAGTCACTTCAATATGCTGTGTCTTATAGGCTCAACACATGGCATC 387
 Db 196 TACGACCGCTTCCTGTGCGGTACCCGAGCGGTCTCATACCCTGGCCGCCAGCGGTGACAG 255

QY 388 ATGAAGATTGTTGCTCAAAATGGTGGCTGTTTGGATACTGGCTTTCTTGGTAAATGGCCCG 447
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 Db 256 CGCGCGGCGAGTGGGAAGATGCTGTGTGTGGTGTCTGCTGCTGCTGTACGGACCA 315
 QY 448 ATGATTCTGGCTTCAGA-----TTCTTGAAGAAGACAGACGAAACAAGGACTGTGAG 501
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 Db 316 GCCATCTTCTGAGCTGGGAGTACCTGTCCGGGGGAGCTCCATCCCGAGGGGCCACTGCTAT 375
 QY 502 CTTGGCTTGTGTACAGAGTGTACATCTCCACATTACAATGCTCTTGGAAATTCCTGCTT 561
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 Db 376 GCGAGTCTCTTACAACTGGTACTTCTCTCATCAGCGCTTCCACCTGGAGTCTTTTACG 435
 QY 562 CTTGTCATCTCTGTGCTTATTTTCAATGTACAGATTTACTGGAGCCTGTGGAAAGCGTAGG 621
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 Db 436 CCCTTCCTCAGCGTCACCTCTTTTAACCTCAGCATCTACCTGAACATCCAGAGGGCGCACC 495
 QY 622 GCTCTCAG 629
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 Db 496 CGCCTCCG 503

RESULT 14
 DA728518 755 bp mRNA linear EST 11-NOV-2005
 LOCUS DA728518 NT2RM2 Homo sapiens cDNA clone NT2RM2001941 5', mRNA
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdn@nifty.com
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute (HRI); cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and HRI.

FEATURES
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 /clone_lib="NT2RM2"
 /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"

ORIGIN

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1 ATCTCCAGATTCCTCTCGTGGGCGCTCTGCAATCCCACTGTATGTACCTCAGTGTGCTGACA 60
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DEFINITION IMAGE:8317348 5', mRNA sequence.
ACCESSION DY313565
VERSION DY313565.1 GI:86996319
KEYWORDS EST.
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 687)
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REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Office of Cancer Genomics
COMMENT Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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FEATURES
source
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varies by clone; ORFs were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBI.presv.dat
a Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match 8.6%; Score 101.2; DB 10; Length 687;
Best Local Similarity 56.1%; Pred. No. 5e-18;
Matches 212; Conservative 0; Mismatches 163; Indels 3; Gaps 1;
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Qy 63 AATGCTCTTCTTTCCTTTGCTATAATGTTAGGCAATGCTGTGCTCATCTTTAGCCTTTGT 122
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306 GACCTTCGCGCGCGCGCTCTGCAAGCTGTGGCTGTAATGAATACCTGATGTGCACATC 365
Qy 300 ATCTGCTCTACAATATTTCTCTCATTTAGCTAGGATCGATACAGTCAAGTTCAAATGCTGT 359
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Qy 360 GTCTTATAGGCTCAACA 377
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Search completed: May 23, 2006, 00:32:30
Job time : 6437 secs
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-626-445-5

Perfect score: 1176

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Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	686.6	58.4	1173	3	US-09-875-076-13
4	172.8	14.7	1239	3	US-09-891-053-2
5	172.8	14.7	2700	3	US-09-891-053-5
6	143.2	12.2	1338	3	US-09-165-543-6
7	143.2	12.2	1953	3	US-09-891-053-26
8	143.2	12.2	3244	3	US-09-165-543-4
9	140.4	11.9	1335	2	US-08-985-090-3
10	140.4	11.9	1335	3	US-09-165-543-3
11	140.4	11.9	1335	3	US-09-167-354-6
12	140.4	11.9	1335	3	US-09-642-855-6
13	140.4	11.9	1335	3	US-09-642-514-6
14	140.4	11.9	1335	3	US-09-642-852-6
15	140.4	11.9	2050	3	US-09-891-053-21
16	140.4	11.9	2685	3	US-09-949-016-5059
17	140.4	11.9	2689	2	US-08-985-090-1
18	140.4	11.9	2689	3	US-09-165-543-1
19	140.4	11.9	2699	3	US-09-167-354-5
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24	94	8.0	1086	3	US-09-165-543-33	Sequence 33, Appli
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27	93.8	8.0	1056	3	US-09-524-162-1	Sequence 1, Appli
28	72.6	6.2	1893	3	US-09-891-053-13	Sequence 13, Appli
29	72.6	6.2	9293	3	US-09-949-016-16801	Sequence 16801, A
30	72	6.1	601	3	US-09-949-016-177027	Sequence 177027,
31	67.6	5.7	1401	3	US-09-826-509-514	Sequence 514, App
32	67.6	5.7	1569	5	US-09-543-679A-2590	Sequence 2590, Ap
33	67.6	5.7	2210	3	US-09-016-434-1177	Sequence 1177, Ap
34	67.6	5.7	2210	3	US-10-166-199-1	Sequence 1, Appli
35	67.6	5.7	6707	5	US-09-543-679A-2593	Sequence 2593, Ap
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38	61.6	5.2	448	3	US-09-891-053-12	Sequence 12, Appli
39	61.2	5.2	1233	3	US-09-721-870-176	Sequence 176, App
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ALIGNMENTS

RESULT 1
US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

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RESULT 3

US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chuen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Query Match 58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 1.6e-201; Indels 9; Gaps 2;
Matches 886; Conservative 0; Mismatches 284;

Qy 1 ATGTGCGAGTCTAACAGTACTTGGCATCTTGGCCACAGCTGCTCAGGTCCCTTGGCATTT 60
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Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTTTCAGAGGTAGACTATCTTCAAGAGAGATCTCT 714
Qy 721 CCTGGATTGAAGGAATCAGCTGCTCATCTCGTCACTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
Db 715 TCTGCATCGACAGAAGTTCTCTGCATCTTCTTCAATTCAGAGAGACAGAGGAAAGAGTAGT 774

QY	781	ATCCTGTGTCCTTTAAGCATCAATGAAACAGCAGTATCACTGCTTCAAGATGGGTTC	840
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QY	841	TTCTGGCGATCGGNAAGTGCAGCGCTTCGCCAAGGAGTACGCAGAGCTTCTCAGAGGC	900
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QY	901	AGGAAGCTAGCAGGTCACCTGGCCATCCTTCTGAGCGCTTTTGCCATTGCTGGGCTCCA	960
Db	895	AGGAGATTAGCAAGTCACTGGCCATTCTCTTAGGGGTTTTTGCTGTGTGCTGGCTCCA	954
QY	961	TACTGTCGTGTCAAAATTGTCCTTTCAACTTACCCAGAAACGGAACGCCCAAAATCGGTG	1020
Db	955	TATTCTGTGTTCAAAATTGTCCTTTCAATTTATTCCTCAGCAACAGGTCCTAAATCAGTT	1014
QY	1021	TGGTACAGCATTTGCCCTTCGGTCGAATGGTTCAATTCGTTTTGTTAATCCCTTCTGTAC	1080
Db	1015	TGSTATAGAATATGCATTTTGCGCTTCAGTGGTTCAAATTCCTTTGTCATCTCTTTGTAT	1074
QY	1081	CTTTTGTCACAGGCGCTTTCAGAAAGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA	1140
Db	1075	CCATTGTGTACAGCGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAGCAA	1134
QY	1141	CCAGCGCTGTACAGAAC---CAGTCAGTATCTTCTTGA	1176
Db	1135	CCTCTACATCAACAACAGTCGGTCAGTATCTCTTAA	1173

```

RESULT 4
US-09-891-053-2
; Sequence 2, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-891-053-2

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	Query Match	14.7%	Score 172.8	DB 3	Length 1239
	Best Local Similarity	49.6%	Prod. No. 9.9e-41		
	Matches 562	Conservative 0	Mismatches 557	Indels 15	Gaps 4
QY	3	GTGGAGCTCAACAGTACTGGCATCTCTGGCCACCAAGCTGCTAGGTCCCTTGGCAATTTT	62		
DB	60	GGGGGCTGCAGGGGGGGCGCGCGCTTCTCGGGTGCCTGGACCGCTGTCTGTGGCTGCGCT	119		
QY	63	AATGTCTTTCATTTTGCCTTTGTCTAAATGGTAGGCAATGCTGTGGTCACTCTTAGCCTTTGT	122		

[illegible]

RESULT 5

US-09-891-053-5
; Sequence 5, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891.053
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (351)...(1589)
; NAME/KEY: misc_feature
; LOCATION: (1)...(2700)
; OTHER INFORMATION: n = A,T,C or G
US-09-891-053-5

Query Match 14.78; Score 172.8; DB 3; Length 2700;
Best Local Similarity 49.66; Pred. No. 1.5e-42;
Matches 562; Conservative 0; Mismatches 557; Indels 15; Gaps 4;
Qy 3 GTGGAGCTTAACAGTACTGTCATCTTTGCCACCAAGCTGCTCAGTCCCTTGGCATTTT 62
Db 410 GGGGCTGACGGGGGGGGGGCTTCTGGCTGCTGACCGCTGCTGCTGGCTGCT 469
Qy 63 AATGCTTCTAATTTGCTTATATGAGGAGCAATGCTGTGCTCATCTTAGCTTTGT 122
Db 470 CATGGCGCTGCTCATCTGTCGCCACAGTACTGGGCAACGCGTGTCTCATGCTCGCTTGT 529
Qy 123 GTGGAGCAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTCTGA 182
Db 530 GGGGATTCGAGCTCGCGCACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGA 589
Qy 183 CTTCCTCGTGGTGTGATTTCCATCTCTGTATACCTCCCTCAGCTGTTTAAAC--TG 239
Db 590 CTTCCTCGTGGTGGCTTCTGTCATCCCATTTGTAGTACCTATGCTGACCGGCGCTG 649
Qy 240 GAATTTTGGAGTGGATCTGCTATGTTTGGCTCATTAAGTACTATCTTTTGTGCAACGC 299
Db 650 GACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTAGTACTACTGCTGTGCTC 709
Qy 300 ATCTGTCTCAATATGCTCTCATTAAGTACGATGATGATGATGATGATGATGATGATG 359
Db 710 CTGGCTCTCAACATCTGCTCATGATGATGATGATGATGATGATGATGATGATGATG 769
Qy 360 GTCTTATAGGCTCAACACACTGCTGATGATGATGATGATGATGATGATGATGATGATG 419
Db 770 CTCTCTAGGGCCAGCAGGGGGGACACGAGACGGGCGCTTCGGAAGATGGCACTGGTGT 829
Qy 420 GATAGTGGCTTCTTGTGTAATAGCCGATGATGATGATGATGATGATGATGATGATGATG 473
Db 830 GGTGCTGGCTTCTTGTGTAATAGCCGATGATGATGATGATGATGATGATGATGATGATG 889
Qy 474 GAACAGCAGCAACAAAGGACTGTGAGCTGGCTTTTGTATACAGTGGTATCATCTCTAC 533

Db 890 CAGTTCCATCCCGAGGGCCACTGCTATGCTAGTCTTCTACAACTGGTACTTTCTCAT 949
Qy 534 CATTACAATGCTCTTGGAAATTCCTGCTTCTGCTGCTATCTCTGCTGCTTATTTCAATGTACA 593
Db 950 CAGGGCTCCACCTCGAGTTCTTCAAGCCCTTCTTCAAGCTTCTTCAACCTCAG 1009
Qy 594 GATTACTGAGCTGTGGAAGCTAGGGCTCTCAGTAGTGTGCTTCAAGCTTCTTCAAGCT 653
Db 1010 CATCTACCTGAACATCCAGAGGGCGCACCCGCTTCTGCTTGTATGGGGCGGTGAGGTGG 1069
Qy 654 CTCACCTACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTCCAGGAC 713
Db 1070 CCAGAACCCCGACAGATGCCAGCCCTCGCACCTCTGAGCTCCCCCAGCTGCTGGG 1129
Qy 714 AAGTAATCTTGGATGAAGGAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773
Db 1130 CTGCTGGCCAAAAGGCGATGGCGAGGCGATGCGCTTGCACAGCTCTGCGAGCTCTCTCAAG 1189
Qy 774 GAGCAGATCTGCTGCTTAAAGGACTACATGACAGCAGTATCACTGCTTCAAGT 833
Db 1190 GGGCAGCTGAGAGGCCAGCTCACTCA---AAAGGGGCTCCAAAGCCATCAGCATCTTCAGC 1246
Qy 834 GGGTTCCTTCTGCGCATCGGAAAGTGCAGCGCTTTCGCAAGGAGGAGTACGAGAGCTTCT 893
Db 1247 ATCCTTGGAGAGCGCATGAAGATGCTGCTCCAGAGCATCACCAGCGCTTCGGCTGTC 1306
Qy 894 CAGAGCAGGAAGCTAGCCAGTCACTGGCCATCTTCTGAGCGCTTTTGGCAATTTGCTG 953
Db 1307 GCGGCAAGAGGTGGCCAGTGGTGGCCATCATGCTGAGCATCTTTGGGCTCTGCTG 1366
Qy 954 GGCTCATACTGCTGTTTCAATGCTCTTCAATGCTCTTCAATGCTCTTCAATGCTCTTCAAT 1013
Db 1367 GGGGCGGTACACGCTCTTAAATGATCATCCAGCTGCTTGGCTGCTGCTGCTGCTGCTGCT 1426
Qy 1014 ATCGGTGTGTACAGCATTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
Db 1427 TT---ACTGTGACAGAGCTCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
Qy 1074 TCTGTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
Db 1484 CCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1537

RESULT 6
US-09-165-543-6
; Sequence 6, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley

Db 961 CATCTACCTGAACATCCAGAGCGCA 986

US-09-165-543-4
; Sequence 4, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 778..2112
; US-09-165-543-4

Query Match 12.2%; Score 143.2; DB 3; Length 3244;
Best Local Similarity 54.2%; Pred. No. 2.2e-33;
Matches 339; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

Qy 3 GTCCGAGCTTAACAGTACTGCGACTTGGCCACACAGCTGCTCAGTCCCTGGCATTTT 62
Db 837 GCGCGCTGACGCGCGCGCGCTTCTCGGCTGCTGACCGCTGCTCTGCTGCGCT 896

Qy 63 AATGCTCTTCATTTTCCCTTTGCTATATAGTGGCAATGCTGTGCTCATCTTAGCCTTTGT 122
Db 897 CATGGCGCTGCTCATCTGCGCCACAGTACTGGGCAACGCGTGTGCTGCTGCGCTTGT 956

Qy 123 GGTGGACAGAAACCTTAGACATCAGAGTAATATTATTTTCTTAATTTGGCTATTCTGA 182
Db 957 GCGGATTGAGCCTCGCGCACCCAGAACAACTTTCTGCTCAACCTCGCATCTCGA 1016

Qy 183 CTTCTCTGCTGGTTTGTATTTCCATTCCTCTGATACCTCCCTCAGCTGTGTTTAAC---TG 239
Db 1017 CTTCTCTGCTGGTGGCTTCTGATCTCCCATTTGATGCTACCTTATGCTGACCGCGCTG 1076

Qy 240 GAATTTTGGAGTGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGC 299
Db 1077 GACCTTCGCGCGCGCGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCTACTGTGTGCTC 1136

Qy 300 ATCTGTCTACAAATATTCTCTCTAGTACGATCGATACAGTCAAGTCTTCAATGCTGT 359
Db 1137 CTGGTCTTCAACATCTGTAATCTCATGAGTATGAGGATTCCTGTGCTCACTCGAGCTGT 1196

Qy 360 GTCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTG 419
Db 1197 CTCCTACAGGGCCAGCAGGGGGACAGAGAGCGGCGCTTCGGAGAGATGGCACTGGTGTG 1256

Qy 420 GATACTGGCTTTCTTGTAAATGCCGATGATTCTGGCTTCAGA-----TTCTTGGAA 473
Db 1257 GGTCTGGCTTCTCTGCTGTATGGCCTGCCATCTGAGTTGGGAGTACCTGTCTGGTGG 1316

Qy 474 GAACAGCAGCAACACAAAGGACTGTGAGCTGCTGGCTTTGTTACAGAGTGGTACATCTCAC 533
Db 1317 CAGTTCCATCCCCGAGGCGCACTGATGCTGAGTTCTTACAACTGGTACTTTCTCAT 1376

Qy 534 CATTACAAATGCTCTTGGAAATTCCTGCTTCTGCTCATCTCTGCTGCTATTTCAATGTACA 593
Db 1377 CACGGCTCCACCTCGAGTTCTTCAGCGCTTCTCAGCGCTTCTCAGCGTTACCTTCTCACTCAG 1436

Qy 594 GATTACTGGAGCCTGTGGAGCGTA 619
Db 1437 CATCTACCTGAACATCCAGAGCGCA 1462

RESULT 9
US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-08-985-090-3

Query Match 11.9%; Score 140.4; DB 2; Length 1335;
Best Local Similarity 53.6%; Pred. No. 1.1e-32;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

; APPLICANT: Lovenberg, Timothy		
; APPLICANT: Erlander, Mark		
; APPLICANT: Pyati, Jayashree		
; APPLICANT: Huvar, Arne		
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3		
; TITLE OF INVENTION: SUBTYPE		
; FILE REFERENCE: JMW		
; CURRENT APPLICATION NUMBER: US/09/167,354A		
; CURRENT FILING DATE: 1998-10-07		
; NUMBER OF SEQ ID NOS: 8		
; SOFTWARE: Patentin Ver. 2.0		
; SEQ ID NO 6		
; LENGTH: 1335		
; TYPE: DNA		
; ORGANISM: Artificial Sequence		
; FEATURE:		
; OTHER INFORMATION: Description of Artificial Sequence:CDNA		
US-09-167-354-6		
Query Match 11.9%; Score 140.4; DB 3; Length 1335;		
Best Local Similarity 53.6%; Pred. No. 1.1e-32;		
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2		
Qy	3	GTCGGAGTCTAACAGTACTGGCATCTTTGCCACCAGCTGCTCAGGTCCTCGATTTTGGCATTTT 62
Db	60	GGCGCGCGCGCGCGCGCGCGCTTCGCGACCTGGACCGCGGTGCTGGCGCGCT 119
Qy	63	AATGCTCTTCATTTGCCCTTGTCTAATAGGTAGGCAATGCTGTGGTCATCTTAGCGCTTGT 122
Db	120	CATGGCGCTGCTCATCGTGGCCAGGTGCTGGGCAACGCGTGTGTCATGCTCGGCTTCGT 179
Qy	123	GGTGGACAGAAACCTTAGACATCGAAAGTAATATTTTTTCTTAATTTGGCTATTTCCTGA 182
Db	180	GGCGGACTCGAGCCTCCGCACCCAGAAACAACCTCTCTCTGCTCAACCTCGCCATCTCGA 239
Qy	183	CTTCTCTGTGGGTTGATTTCCATTCTCTGTGTACATCCCTCACGTTTG---TTTAACTG 239
Db	240	CTTCTCTGTGGGCGCCTTCTGTCATCCCACTGATGTATGATCCCTACGTCGACAGGCCGCTG 299
Qy	240	GAATTTTGGAAGTGGAATCTGTCATGTTTGGCTCATTACTGACTATCTTTTGTGCACGCG 299
Db	300	GACCTTCGGCGGGCCCTCTGCAAGCTTGGCTGGTAGTGACTTACCTGCTGTGCACTC 359
Qy	300	ATCTGTCTCAATATGTCCTCATTTAGTAGCATCGATACGATACAGTTCAGTTTCAAAATGCTGT 359
Db	360	CTCTGCGCTTCAACATCGTGTGTCATCAGCTACGACCGCTTCTGTGCGGTCACTCCGAGCGGT 419
Qy	360	GTCTTATAGGSGCTCAACACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTG 419
Db	420	CTCATACGGGGCCACGAGGCTGACACGGCGGGCGAGTCGGGAAGATGCTGTGGTGTG 479
Qy	420	GATACCTGGCTTTCTTTGGTAAATGSCCGCATGATTCCTGGCTTCAGAT-----TCTTGGAA 473
Db	480	GGTGCTGGCCTTCTCTGTGTACGACACAGCCATCCTGAGCTGGGAGTACCTGTCCGGGG 539
Qy	474	GAACAGACAGAAACAACAAGACTGTGAGCTGGCTTTGTTTACAGAGTGTACATCTCAC 533
Db	540	CAGCTCCATCCCCGAGGGCCACTGCTATGCGAGTTCTTCTACAACTGGTACTTTCCTCAT 599
Qy	534	CATTACAAATGCTCTTTGGAAATTCCTGCTTCCTGTCTCATCTCTGTGGCTATTATTCAATGTACA 593
Db	600	CACGGCTTCCACCTGGAGTTCTTTACGCCCTTCTCAGCGGTACCTTCTTTAACTTCAG 659
Qy	594	GATTTACTGAGCCTGTGGAAAGCGTAGGGCTCTCAG 629
Db	660	CATCTACTGAAACATCCAGAGGGCCACCCGCGCTCCG 695

RESULT 12
US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:

:	APPLICANT:	Lovenberg, Timothy
:	APPLICANT:	Erlander, Mark
:	APPLICANT:	Pvati, Jayaashree
:	APPLICANT:	Huvar, Arne
:	TITLE OF INVENTION:	DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
:	TITLE OF INVENTION:	SUBTYPE
:	FILE REFERENCE:	JMW
:	CURRENT APPLICATION NUMBER:	US/09/642,855
:	CURRENT FILING DATE:	2000-08-21
:	PRIOR APPLICATION NUMBER:	09/167,354
:	PRIOR FILING DATE:	1998-10-06
:	NUMBER OF SEQ ID NOS:	8
:	SOFTWARE:	PatentIn Ver. 2.0
:	SEQ ID NO 6	
:	LENGTH:	1335
:	TYPE:	DNA
:	ORGANISM:	Artificial Sequence
:	FEATURE:	
:	OTHER INFORMATION:	Description of Artificial Sequence:CDNA
:	US-09-642-855-6	
	Query Match	11.9%; Score 140.4; DB 3; Length 1335;
	Best Local Similarity	53.6%; Pred.No.1.le-32;
	Matches 341; Conservative	0; Mismatches 286; Indels 9; Gaps 2;
Qy	3	GTCGGAGCTCAACAGTACTCGCATCTTGCCACACAGCTGCTCAGGTGCCCTTGGCATTTTT 62
Db	60	GGCGGCGGGGGGGGGCGCGCTTCTCGGCAGCTGACC GGCGGTGCTGGCGCGCT 119
Qy	63	AATGCTCTTCAATTGGCTTTGCTATAATGTTAGGAATGCTGTGGTCACTTTTAGCTTTGT 122
Db	120	CATGGCGCTGCTCATCGTGGCCACGGTGTCTGGGCACACGCGTGTCTA GTCTCGCTTCGT 179
Qy	123	GGTGGACAGAAAACTTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCTGA 182
Db	180	GGCGGACTCGAGGCTCGGCACCAGAACAACTTCTTCTGCTCAA CTGCGCATCTCGA 239
Qy	183	CTTCTCTGTGGGTTTGATTTCCAATCTCTGTATACATCCCTCACGTTG ---TTTAACTG 239
Db	240	CTTCTCTGTGGCGGCTTCTGCACTCCACCTGTATGACCC TACGCTGACAGGCGCTG 299
Qy	240	GAATTTTGGAGTGAATCTGCATGTTTGGCTCAITACTGACTATCTTTTGTGCACGCG 299
Db	300	GACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGAGTACTCTGCTGTGCACCTC 359
Qy	300	ATCTGTCTACAATATTTGCTCTCAATTAGTACGATACGATACAGTCAGTTTCAAATGCTGT 359
Db	360	CTCTGCTTCAACATCGTGTCTCATAGTACGACCGCTTCTCTGTGCGTCA CCGAGCGGT 419
Qy	360	GTCTTATAGGGCTCAACACNCTGGCATCATGAAGATTGTTGCTCAATGTGGCTGTTTG 419
Db	420	CTCATACCGGGCCAGCAGGGGTGACACGCGGGGGCAGTGC GAAGAATGCTGTGGTGTG 479
Qy	420	GATACCTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGAT -----TCTTGGAA 473
Db	480	GGTGTCTGGCTTCTCTGTATCGGACCGACCATCTTGAGCTGGAGTACCTGTCCGGGGG 539
Qy	474	GAACAGCAGAAACAAAAGGACTGTGAGCGCTGGCTTTGTTACAGATGGGTACATCCTCAC 533
Db	540	CAGCTCCATCCCCAGGGGCCACTGCTATGCCAGATTCTTCTACAACTGGTACTTCTCAT 599
Qy	534	CATTACAATGCTCTTGGAAATTCCTGCTTCTGTGTCATCTCTGTGGCTTATTTTCAATGTACA 593
Db	600	CACGGTTCACCTUGAGTTCTTTACGCCCTTCTCAGGCTCACCTTCTTTAACCTCAG 659
Qy	594	GAATTTACTGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
Db	660	CATCTACCTGAAATCCAGAGGGCGACCGGCGCTCCG 695

RESULT 13
US-09-642-514-6
; Sequence 6, Application US/09642514

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; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-514-6

Query Match      11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 1.1e-32;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCCGAGCTTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCAATTTT 62
Db 60 GCGCGCGCGGGCGCGCGCGCTTCTCGGAGCTGGACCGCGGTGTCGGCGCGCT 119
Qy 63 AATGCTTTCAATTTGCCCTTGTCTATAATGTTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122
Db 120 CATGGCGCTGCTCATCTGTGGCCACGGTGTGGGCAACGGCGTGTCTCGCTTCGT 179
Qy 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTCTCGA 182
Db 180 GGCGGACTCGAGCTCGCGCACCCAGAACAACTTCTCTGCTCAACCTCGCATCTCCGA 239
Qy 183 CTTCCTGTGGTGTGATTTCCATCTCTGTGTAATCCCTCACCTGTG---TTTAACTG 239
Db 240 CTTCCTGTGGCGCCCTTCTGCATCTCCACCTATGTATGTAACCTACGTGTGACAGCGCGTG 299
Qy 240 GAATTTTGGAGTGGAATCTGCAATGTTTGGCTCAATTAAGTACTATCTTTTGTGCACCGC 299
Db 300 GACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGGTAGTGAATCTCTGTGTGCACTC 359
Qy 300 ATCTGTCTACAATATTTGCTCTCAATAGCTACGATCGATACAGTCAAGTTCAAATGCTGT 359
Db 360 CTCTGCTTCAACATCTGCTCATCAGCTACGACCGCTTCTGTGCGGTACCCGAGCGGT 419
Qy 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTG 419
Db 420 CTCATACCGGGCCAGCAGGGTGACACGCGCGGGCAGTGGGAAGATGCTGTGGTGTG 479
Qy 420 GATACTGGCTTTCTTGTGTAATGGCCCGATGATCTGGCTTCAGAT-----TCTTGGAA 473
Db 480 GGTGCTGGCTTTCTGCTGTACGACACGACCATCTTGAGCTGGAGTACCTGTCCGGGG 539
Qy 474 GAACAGCAGCAACAAAGGACTGTGAGCTTGGCTTTGTTTACAGAGTGGTACATCTCTAC 533
Db 540 CAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTTACAACTGGTACTTCTCTCAT 599
Qy 534 CATTAATAGTCTTTGNAATCTCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593
Db 600 CACGGCTTCCACCTGGAGTTCTTTACGCGCTTCTCAGCGCTTCTCAGCGTCACTTCTTTAACCTCAG 659
Qy 594 GATTTACTGGAGCTGTGGAGCGTAGGGCTCTCAG 629
Db 660 CATCTACTGAACATCCAGAGGCGCACCCGCTCCG 695
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US-09-642-852-6
; Sequence 6, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JWJ
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-852-6

Query Match      11.9%; Score 140.4; DB 3; Length 1335;
Best Local Similarity 53.6%; Pred. No. 1.1e-32;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCCGAGCTTAACAGTACTGGCATCTTGGCCACAGCTGCTCAGTCCCTTGGCAATTTT 62
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Qy 63 AATGCTTTCAATTTGCCCTTGTCTATAATGTTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122
Db 120 CATGGCGCTGCTCATCTGTGGCCACGGTGTGGGCAACGGCGTGTCTCGCTTCGT 179
Qy 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTCTCGA 182
Db 180 GGCGGACTCGAGCTCGCGCACCCAGAACAACTTCTCTGCTCAACCTCGCATCTCCGA 239
Qy 183 CTTCCTGTGGTGTGATTTCCATCTCTGTGTAATCCCTCACCTGTG---TTTAACTG 239
Db 240 CTTCCTGTGGCGCCCTTCTGCATCTCCACCTATGTATGTAACCTACGTGTGACAGCGCGTG 299
Qy 240 GAATTTTGGAGTGGAATCTGCAATGTTTGGCTCAATTAAGTACTATCTTTTGTGCACCGC 299
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Qy 360 GTCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTG 419
Db 420 CTCATACCGGGCCAGCAGGGTGACACGCGCGGGCAGTGGGAAGATGCTGTGGTGTG 479
Qy 420 GATACTGGCTTTCTTGTGTAATGGCCCGATGATCTGGCTTCAGAT-----TCTTGGAA 473
Db 480 GGTGCTGGCTTTCTGCTGTACGACACGACCATCTTGAGCTGGAGTACCTGTCCGGGG 539
Qy 474 GAACAGCAGCAACAAAGGACTGTGAGCTTGGCTTTGTTTACAGAGTGGTACATCTCTAC 533
Db 540 CAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTTACAACTGGTACTTCTCTCAT 599
Qy 534 CATTAATAGTCTTTGNAATCTCTGCTTCTGCTCATCTCTGCTGCTTATTTCAATGTACA 593
Db 600 CACGGCTTCCACCTGGAGTTCTTTACGCGCTTCTCAGCGCTTCTCAGCGTCACTTCTTTAACCTCAG 659
Qy 594 GATTTACTGGAGCTGTGGAGCGTAGGGCTCTCAG 629
Db 660 CATCTACTGAACATCCAGAGGCGCACCCGCTCCG 695
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RESULT 15

US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, HIRAKU
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohca, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)...(1629)
US-09-891-053-21

Query Match 11.9%; Score 140.4; DB 3; Length 2050;
Best Local Similarity 53.6%; Pred. No. 1.3e-32;
Matches 341; Conservative 0; Mismatches 286; Indels 9; Gaps 2;

Qy 3 GTCCGAGTCTAACAGTAGTCTGCGCATCTTGCACACAGCTGCTCAGGTCCCTTGGCATTTT 62
Db 330 GCGCGCGCGCGCGCGCGCGCGCTTCTCGGAGCTTGGACCGCGTGTGGCGCGCT 389

Qy 63 AATGCTTTCATTTTGCCTTGTCTATAATGGTAGGCAATGCTGTGCTCATCTTAGCCTTTGT 122
Db 390 CATGGCGCTGCTCATGCTGGCCACGGTGTGGGCAACGGCTGCTCATGCTCGCCTTCGT 449

Qy 123 GGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTGA 182
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Qy 300 ATCTGTCTACAATATGTCCTCATTAAGTACGATCGATACAGTCAAGTTCAAATGCTGT 359
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Db 690 CTCATACCGGGCCAGCAGGGGTGACACCGCGCGGCGAGTGGGAAGATGCTGTGGTGTG 749

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Db 750 GGTGCTGGCCTTCTGTGTCAGGACCAAGCATCTGAGCTGGAGTACCTGTCCGGGG 809

Qy 474 GAACAGCACGAAACAAAGGACTGTGAGCCTGCTGTTGTTTACAGAGTGGTACATCTCAC 533
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Db 870 CAGGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTTACAGGTCACCTTCTTTAACCTCAG 929
Qy 594 GATTTACTGGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
Db 930 CATCTACCTGAACATCCAGAGGCGCACCCCGCTCCG 965

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Job time : 267 secs

GenCore version 5.1.8
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1176	100.0	1176	9	US-10-626-445-5
2	1176	100.0	1176	10	US-10-626-126-5
3	1176	100.0	1176	10	US-10-626-398-5
4	958.4	81.5	1176	9	US-10-626-445-6
5	958.4	81.5	1176	10	US-10-626-126-6
6	958.4	81.5	1176	10	US-10-626-398-6
7	686.6	58.4	1173	3	US-09-812-216-1
8	686.6	58.4	1173	3	US-09-910-411-1
9	686.6	58.4	1173	3	US-09-875-076-13
10	686.6	58.4	1173	3	US-09-876-252-13
11	686.6	58.4	1173	6	US-10-052-193-1
12	686.6	58.4	1173	7	US-10-272-983-13
13	686.6	58.4	1173	7	US-10-354-769-1
14	686.6	58.4	1173	7	US-10-393-807-13
15	686.6	58.4	1173	7	US-10-417-820A-13
16	686.6	58.4	1173	8	US-10-349-253A-1
17	686.6	58.4	1173	8	US-10-723-955-13

ALIGNMENTS

RESULT 1
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Query Match	100.0%	Score 1176;	DB 9;	Length 1176;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1176;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	ATGTCGGAGTCTAACAGTACTGGCATCTTCCACACAGCTGCTCAGGTCCTCCCTTGGCAATTT	60	
Qy	61	TTAATGCTTCATTTGGCTTTGCTTATTAATGTTAGGCAATGCTGTGGTCACTTAGCCTTT	120	
Db	61	TTAATGCTTCATTTGGCTTTGCTTATTAATGTTAGGCAATGCTGTGGTCACTTAGCCTTT	120	
Qy	121	GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTC	180	
Db	121	GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTC	180	
Qy	181	GACTTCCTCGTGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG	240	

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601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCTTACAGAGTGGTACATCTCCACT 660
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RESULT 2
US-10-626-126-5
; Sequence 5, Application US/10626126
; Publication No. US2005007470A1
; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Query Match 100.0%; Score 1176; DB 10; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1141 CCAGCGCTGTCCAGAACCAAGTCAGTATCTTCTTGA 1176
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RESULT 3

US-10-626-398-5

; Sequence 5, Application US/10626398

; Publication No. US20050074841A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

; FILE REFERENCE: PRD-0034

; CURRENT APPLICATION NUMBER: US/10/626,398

; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849

; PRIOR FILING DATE: 2001-02-22

; PRIOR FILING DATE: 2000-05-31

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5

; LENGTH: 1176

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-626-398-5

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Query Match 100.0%; Score 1176; DB 10; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTGGAGTCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCCTTTGGCATTT 60
Db 1 ATCTGGAGTCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCCTTTGGCATTT 60
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RESULT 4

US-10-626-445-6

; Sequence 6, Application US/10626445

; Publication No. US20040248252A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

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Db 721 CCTGGAATGAAGAAATCAGTGCATCTCGTCACTCAGAAAAAGTCTCTGAAAGAGAGCAGC 780
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Db 901 AGGAAGCTAGCCAGGTCTGCGCATCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
QY 961 TACTGTCTGTTCACAAATGTCCTTCAACTTACCCAGAGAGGACGCCCAAAATCGGTG 1020
Db 961 TACTGTCTGTTCACAAATGTCCTTCAACTTACCCAGAGAGGACGCCCAAAATCGGTG 1020
QY 1021 TGGTACAGCAATGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
Db 1021 TGGTACAGCAATGCTTCTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080
QY 1081 CCTTTGTGTACAGGCGTTTCCAGAAAGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
Db 1081 CCTTTGTGTACAGGCGTTTCCAGAAAGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140
QY 1141 CCAGCGCTGTCCAGAACCAAGTCAGTATCTTCTTGA 1176
Db 1141 CCAGCGCTGTCCAGAACCAAGTCAGTATCTTCTTGA 1176
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RESULT 4

US-10-626-445-6

; Sequence 6, Application US/10626445

; Publication No. US20040248252A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype


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; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Query Match      81.5%; Score 958.4; DB 9; Length 1176;
Best Local Similarity 88.4%; Pred. No. 7.4e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCACACAGCTGCTCAGGTGCCCTTGGCAATT 60
DB 1 ATGTCGGAGTCTAACGGCACTGACGCTTTCGCCACTGACTGCTCAAGTCCCTTGGCAATT 60
QY 61 TTAATGTCTTTCAATTGCTTTTGTCTATAAAGTAGGCAATGCTGTGGTCAATTTAGCCTTT 120
DB 61 TTAATGTCCCTGTCTTGTCTTTGTCTATAAAGTAGGCAATGCTGTGGTCAATTTAGCCTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
DB 121 GTAGACAGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
QY 181 GACTTCTCTGTGGTGTGATTTCCATTCCTCTGATCATCCCTCAGCTGTGTTTAAGTGG 240
DB 181 GACTTCTCTGTGGTGTGATTTCCATTCCTCTGATCATCCCTCAGACGCTGTTTAAGTGG 240
QY 241 AATTTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
DB 241 AATTTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
QY 301 TCTGTCTACAATATGTCTCTATAGTAGATCGATACACAGTCAGTTCCTCAATGTCTGTG 360
DB 301 TCCGTCTACAGTATGTCTCTATAGTAGATCGATACACAGTCAGTTCCTCAATGTCTGTG 360
QY 361 TCTTTATAGGCTCAACACACTGTCATCATGAAGATTGTCTCAATGTGGCTGTTTGG 420
DB 361 CGTTATAGACACAGACACTGGCATCTGAAATTTGTTGCTCAATGTGGCTGTTTGG 420
QY 421 ATACTGGCTTTCTTGGTAAATGSCCGGATGATTTCTGGCTTCAGATTTCTTGGAAAGACGC 480
DB 421 ATACTGGCTTTCTTGGTCAATGSCCGCAATGATTTCTGGCTTCGGATTTCTTGGAAAGACGC 480
QY 481 ACGAACAAGAGACTGTGAGCCCTGGCTTTGTACAGAGTGGTACATCCCTCACCATTACA 540
DB 481 ACCAACAACAGAGAGTGCAGGCTGGCTTTGTACTGAGTGGTACATCTCCGCAATTACA 540
QY 541 ATGCTCTTGGAAATCTCTGTCTCTGATCATCTCTGTGCTTTATTTCAATGACAGATTTAC 600
DB 541 GCATTTCTTGGAAATCTCTGTCTCTGATCATCTCTGTGCTTTATTTCAATGACAGATTTAC 600
QY 601 TGGAGCCTGTGGAGCGTGGAGTCTCAGTAGGTGGCTTAGCCAGCTGGATTTCTCCACT 660
DB 601 TGGAGCCTGTGGAGCGTGGAGTCTCAGTAGGTGGCTTAGCCAGCTGGATTTCTCCACT 660
QY 661 ACCTTTCCAGTGTTCAGAGACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
DB 661 ACCTTTCCAGGGGCACTGAGACACTCAGCAGAACTGGGTGGCTTGTAGGACAAGTCTT 720
QY 721 CCGTGAATTGAAGGAATCAGCTGATCTCTGCTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
DB 721 CCGTGAATTGAAGGAATCAGCTGATCTCTGCTCACTCAGAAAGTCTCGAAGAAAGAGCAGT 780
QY 781 ATCCTGGTGTCTTAAAGGACTCAGTGAACAGCAGATATCACTGCCCTCAAAGTGGGTTC 840
DB 781 ATCCTGGTGTCTTAAAGGACTCAGTGAACAGCAGATATCACTGCCCTCAAAGTGGGTTC 840
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DB 781 CTCTGGTGTCTTAAAGGACTCAGTGAAGGGTAGTATCATCGCCTTCAAAGTGGGTTC 840
QY 841 TTCTGGCGATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGGC 900
DB 841 TTCTGGCGATCGAAAGCGCCAGTGTCTTCCAGAGAGAGACACGTGGAGCTTCTCAGAGGC 900
QY 901 AGGAAGCTAGCCAGGTCACTGGCCATCTTCTTGAGCGCTTTTGGCCATTTGCTGGGTCCA 960
DB 901 AGGAAGCTAGCCAGGTGCTAGTGTCTCTGAGTGTCTTGGCCATTTGCTGGGTCCG 960
QY 961 TACTGTCTGTTCACAATTTGCTTCAACTTACCCAGAGAGCGCCCAATCGGTG 1020
DB 961 TATTGCTGTTCACAATTTGCTTCAACTTATCGAGAGGGAGCGCCCAATCGATT 1020
QY 1021 TGTACAGCATTTGCCCTTCTGGCTGCAATGTTCAATTTGTTTCTTAATCCCTTCTGTAC 1080
DB 1021 TGTACAGCATGACCTTTTGGCTACAGTGTTCATTTCACTTATTAATCCCTTCTTATAC 1080
QY 1081 CCTTTGTGTACAGGCGTTTCCAGAAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140
DB 1081 CCTTTGTGTACAGAGCGTTTCCAGAAAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140
QY 1141 CAGCGCTGTACAGAAACAGTCAGTATCTTCTTGA 1176
DB 1141 CCAGCACTTTCAGACACCCAGTCAGTATCTTCTTGA 1176

RESULT 5
US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changle
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Query Match      81.5%; Score 958.4; DB 10; Length 1176;
Best Local Similarity 88.4%; Pred. No. 7.4e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCACACAGCTGCTCAGGTGCCCTTGGCAATT 60
DB 1 ATGTCGGAGTCTAACGGCACTGACGCTTTCGCCACTGACTGCTCAAGTCCCTTGGCAATT 60
QY 61 TTAATGTCTTTCAATTGCTTTTGTCTATAAAGTAGGCAATGCTGTGGTCAATTTAGCCTTT 120
DB 61 TTAATGTCCCTGTCTTGTCTTTGTCTATAAAGTAGGCAATGCTGTGGTCAATTTAGCCTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
QY 181 GACTTCTCTGTGGTGTGATTTCCATTCCTCTGATCATCCCTCAGCTGTGTTTAAGTGG 240
DB 181 GACTTCTCTGTGGTGTGATTTCCATTCCTCTGATCATCCCTCAGACGCTGTTTAAGTGG 240
QY 241 AATTTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGTGCACCGCA 300
DB 241 AATTTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
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QY 301 TCTGTCTACAAATATGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAATGCTGTG 360
Db 301 TCCGTCTACAGATATGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAACGCTGTG 360
QY 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAATGGTGGCTGTTTGG 420
Db 361 CGTTATAGAGCACACACACTGGCATCTCTGAAATTTGTGCTCAAATGGTGGCTGTTTGG 420
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTCTTGGGAAGAACAGC 480
Db 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCGGATTCTTGGGAAGAACAGC 480
QY 481 ACGAACACAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540
Db 481 ACCAACACAAGGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCCTGCCATTACA 540
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Db 541 GCATCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGTGTCTATTTCAAGTGTACAGATTTAC 600
QY 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTTCATCGCT 660
Db 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTTCATCGCT 660
QY 661 ACCTTCTCAGTGTCTTAGGACACTTACACAGAGTGGGTGGCTTGCAGGACAGCAAGTAAT 720
Db 661 ACCTTCTCAGGCGCACTGGACACTCAGCGCAAACTGGGTGGCTTGTAGGACAAAGTCTT 720
QY 721 CCTGGATTGAAGGAATCAGCTGTCATCTGTCACCTCAGAAAGTCTCCGAAGAAAGAGCAGC 780
Db 721 CCTGGATTAAAGGAACACAGCGCATCTCTTCAATTCAGAAAGTCCAGGAGAAAGAGCAGT 780
QY 781 ATCTGTGTCTTTAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840
Db 781 CTCCTGGTGTCTTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGAGTAGCGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCAGAAAGCCAGTGTCTTACCAGAGAGACGCTGGAGCTTCTCAGAGGC 900
QY 901 AGGAAGCTAGCAGCTCACTGGCCATCTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
Db 901 AGGAAGCTAGCAGCTCACTGAGCTGTCTCTGAGTGTCTTGGCATTTGCTGGGCTCCG 960
QY 961 TACTGTCTGTTTCAAAATGTCCTTTCAACTTACCCAGAAAGCGAACGCCCAAAATCGGTG 1020
Db 961 TATTGCTGTTTCAAAATGTTCTTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT 1020
QY 1021 TGGTACAGCATGCTTCTGGCTGCAATGGTTCATTTGTTTAAATTCCTTTCTGTAC 1080
Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTTCACTTATTAATCCCTTTCTATAC 1080
QY 1081 CCTTTGTGCACAGCGCTTCCAGAGCGTTTCTGGAAGTACTTTCTGTGACAAAGCAA 1140
Db 1081 CCTTTGTGCCACAGCGTTTCCAGAGCGTTTCTGGAAGTACTTTCTGTGACAAAGCAA 1140
QY 1141 CCAGCGCTGTGCACAGAACCACTCAGTATCTCTTGA 1176
Db 1141 CCAGCACTTTCACAGAACCACTCAGTATCTCTTGA 1176
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RESULT 6

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US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
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; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6
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Query Match 81.5%; Score 958.4; DB 10; Length 1176;

Best Local Similarity 88.4%; Pred. No. 7.4e-291;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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QY 1 ATGTGCGAGTCTAAACAGTACTGGCATCTTGGCACAGCTGCTCAGGTCCCTTGGCAATT 60
Db 1 ATGTGCGAGTCTAAACGACCTGACGTCTTGGCACTGACTGCTCAAGTCCCTTGGCAATT 60
QY 61 TTAATGCTTTCATTTGGCTTTGCTTATTAATGGTAGGCAATGCTGTGGTCAATCTTAGCCCTTT 120
Db 61 TTAATGCTCCCTGCTTGTCTTTGCTTATTAACGATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120
QY 121 GTGCTGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
QY 181 GACTTCTCTGGTGGGTTTGATTTCATTTCCATTCCTGTACATCCCTCAGCTGTGTTTAACTGG 240
Db 181 GACTTCTCTGGTGGGTTGTCATCTCCATTCCTGTACATCCCTCAGCTGTGTTTAACTGG 240
QY 241 AATTTTGGAAAGTGGAAATCTGCATGTTTGGCTCAATTAATGACTATCTTTTGTGCAACCGCA 300
Db 241 AATTTTGGAAAGTGGAAATCTGCATGTTTGGCTCAATTAATGACTATCTTTTGTGCAACCGCA 300
QY 301 TCTGTCTACAAATATGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAATGCTGTG 360
Db 301 TCCGCTCTACAGTATTTGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAACGCTGTG 360
QY 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAATGCTGGCTGTTTGG 420
Db 361 CGTTTATAGAGCACAGACACACTGGCATCTGAAATTTGTGCTCAAATGCTGGCTGTTTGG 420
QY 421 ATACTGCTTCTTGGTAAATGGCCGATGATTTCTGCTTCAGATTCTTGGGAAGAACAGC 480
Db 421 ATACTGCTTCTTGGTAAATGGCCGATGATTTCTGCTTCGGATTCTTGGGAAGAACAGC 480
QY 481 ACGAACACAAGGACTGTGAGCTGGCTTTGTTACAGAGTGGTACATCTCACCATTACA 540
Db 481 ACCAACACAAGGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCCTGCCATTACA 540
QY 541 ATGCTCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Db 541 GCATCTTGGAAATTCCTGCTTCTGTCATCTCTGTGGTGTCTATTTCAAGTGTACAGATTTAC 600
QY 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTTCCAAT 660
Db 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTTCATCGCT 660
QY 661 ACCTTCTCAGTGTCTTAGGACACTTACACAGAGTGGGTGGCTTGCAGGACAGCAAGTAAT 720
Db 661 ACCTTCTCAGGCGCACTGGACACTCAGCGCAAACTGGGTGGCTTGTAGGACAAAGTCTT 720
QY 721 CCTGGATTGAAGGAATCAGCTGTCATCTGTCACCTCAGAAAGTCTCCGAAGAAAGAGCAGC 780
Db 721 CCTGGATTAAAGGAACACAGCGCATCTCTTCAATTCAGAAAGTCCAGGAGAAAGAGCAGT 780
QY 781 ATCTGTGTCTTTAAGGACTCACATGAACAGCAGTATCACTGCTTCAAAGTGGGTTC 840
Db 781 CTCCTGGTGTCTTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAAGGAGTAGCGAGCTTCTCAGAGGC 900
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PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/151,114
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/108,029
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 1173
TYPE: DNA
ORGANISM: Homo sapiens
US-09-876-252-13

Query Match 58.4%; Score 686.6; DB 3; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

QY 1 ATGTCGAGTCTAACAGTCTGCGATCTTCCACCGCTGCTCAGTCCCTTGGCATTT 60
DB 1 ATGCCAGATCTAATAGCAATCAATTTATCTAGCACTCGTGTACTTTAGCATTT 60
QY 61 TTAATGTCTTCAATTTGCTTTGCTTAATAGTGGCAATGCTGTGTCATCTTAGCCCTT 120
DB 61 TTTATGTCCTTAGTACTTTTGTATTAATGCTAGGAATGCTTTGGTCAATTTAGCTTTT 120
QY 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTTTTCTTAATTTGGCTATTCT 180
DB 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTTTTCTTAATTTGGCTATTCT 180
QY 181 GACTTCTCGTGGTGTGATTTCCATCTCTGTACATCCCTCAGCTGTGTGTTAAGTGG 240
DB 181 GACTTCTCGTGGTGTGATTTCCATCTCTGTACATCCCTCAGCTGTGTGTTAAGTGG 240
QY 241 AATTTTGGAAAGTGAATCTCATGTTTGGCTCAATTAAGTACTATCTTGTGTCACCGCA 300
DB 241 GATTTTGGAAAGGAAATCTGTATTTGGCTCACTACTACTACTATCTGTATGTACAGCA 300
QY 301 TCTGTCTACAATATTTGCTCATTTAGTACGATACGATACAGTCAAGTTCAAAATGCTGTG 360
DB 301 TCTGTATATAAATTTGCTCATCTAGTATGATGATACCTGTGCTCAGTCTCAAAATGCTGTG 360
QY 361 TCTTATAGGCTCAACACATGGCATCAAGATTTGCTCAATTTGGCTGCTGTTTGG 420

DB 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
QY 421 ATACTGCTTTCTTGGTAAATGGCCCGATGATCTTGGCTTCTGATTTCTTGGAAAGCAAGC 480
DB 421 GTGCTGGCTTCTTGTAGTGAATGGCCCAATGATTTCTAGTCTTCTTGGAAAGCA---- 476
QY 481 ACGAACACAAAGGACTGTGAGCCTGCTTGTGTACAGAGTGGTGTACATCTCCACCATACA 540
DB 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTATATCTCTTGGCCATACA 534
QY 541 ATGCTCTTGGAAATTTCTGCTTCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTAC 600
DB 535 TCATTTCTTGGAAATTCGTGATCCCGATCATCTAGTCTGCTTATTTCAACATGATTTAT 594
QY 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGATTTCTCCACT 660
DB 595 TGGAGCCTGTGGAAGCGTAGTATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654
QY 661 ACCTCTTCCAGTCTTCCAGGACATTTACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
DB 655 GTCTCTTCCAAACATCTGTGACATCTCAATCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 721 CCTGGATTGAAGGAATCAGCTGCTGCTCCTCAGTCAAGAACTCTCAGAAAGAGGAGC 780
DB 715 TCTGCATCGACAGAGTCTCTGATCTCTTCAATTCAGAGACAGAGAGAGAGTAGT 774
QY 781 ATCTGTGTCTTAAAGGACTCAATGAACAGAGTATCACTGCTTCAAAAGTGGGTTC 840
DB 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTTC 834
QY 841 TTCTGGCGATCGGAAGTGCAGCGCTTCGCCAAGGAGTACGAGCTTCTCAGAGGC 900
DB 835 TTCTCCCAATCAGATTTCTGTAGCTTCTTCAACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
QY 901 AGGAAGTAGCAGGCTCAGTGGCCATCTTCTGAGCGCTTTTGGCCATTTGCTGGGCTCCA 960
DB 895 AGGAGATTAGCCAAAGTCTGAGCTTCTTAGGGCTTTTGGCTTTGCTGGGCTCCA 954
QY 961 TACTGTCTGTCAATTTGCTTCAATTTCACTTCCAGAAAGGCTTCTTGGAAAGTACTTTGTGACAAAGCAA 1140
DB 955 TATTCTCTGTCAATTTGCTTCTTCAATTTTCTTCTCAGCAACAGGCTCTTAATTCAGTT 1014
QY 1021 TGGTACAGCATTCCTTCTGGCTGCAATGTTCAATTCGTTTGTATTCCTTCTCTGATC 1080
DB 1015 TGGTATAGAAATTCATTTTGGCTTCAAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074
QY 1081 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTTGGAAAGTACTTTGTGACAAAGCAA 1140
DB 1075 CCATTTGTGTACAGGCGTTTCAAAAGGCTTCTTGAAGATATTTTGTATATAAAGCAA 1134
QY 1141 CCAGCGCTGTACAGAAC---CAGTCAAGTATCTTTTGA 1176
DB 1135 CCTCTACCATCAACACAGCTGCTGCTCAGTATCTTCTTAA 1173

RESULT 11
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens


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181 GACTTCCTTTGGGGTGAATCTCCATTCCTTTGATACCTCCACAGCTGTTGCAATGG 240
241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCAATTAAGTACTATCTTTTGTGCAACGCCA 300
241 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
301 TCTGCTACAAATATGTCCTCAATTAGCTACGATCGATACCAAGTCAGTTTCAAAATGCTGTG 360
301 TCTGTATATAACATTTGCTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420
361 TCTTATAGAACTCAACATACTGGGGCTTGAAGATTGTTACTCTGATGTTGGCGGTTGG 420
421 ATACTGCTTCTTTGGTAAATGGCCCGAATGATTCGCTGTTTCAAGATCTTTTGAAGAACAGC 480
421 GTGCTGCTCTTCTTGTGAAATGGGCCAATGATTCAGTCTTTCAGAGTCTTGAAGGA---- 476
481 ACGAACACAAGGACTCTGAGCCTGGCTTGTTCAGAGTGGTACATCCTCACCAATTACA 540
477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATACATCCTTGGCCATCACA 534
541 ATGCTCTTGAATTCCTGCTTCCCTGCTCATCTCTGCTGCTTATTTCAATGTACAGATTAC 600
535 TCATTCTTGAATTCGTGATCCCGAGTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATGCTGGATTCTCCOACT 660
595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGTGCCCAAGGCCATCCTGGAGTACTGCT 654
661 ACCTCTTCCAGTGTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
655 GTCTCTTCCAACTCTCTGGACACTCATCTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
721 CCTGGATTGAAGGAATCAGCTGCTATCTGCTCAGTACAGAAATGCTCCTCAAGAAAGAGCAGC 780
715 TCTGCATCGAAGAAATCTCTGCACTCTTCAATTCAGAGAGACAGAGGAAAGAGTAGT 774
781 ATCTGCTGTCTTAAAGGACTCAGATGAACAGCAGATATCACTGCTTCAAAAGTGGGTTC 840
775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAATTCCTTCAAAATGGGTTC 834
841 TTTCTGGCGATCGGAAGTGAAGCTGCTGCGCAAGAGGAGTAGCAGAGCTTCTCAGAGGC 900
835 TTTCTCCAAATCAGATTCTGTAGCTCTTCAAGAAAGGGAACATGTGAACCTGCTTAGAGCC 894
901 AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA 960
895 AGGAGATTGCCAAGTCACTGGCCATCTCTTAGGGGTCTTGTGTTGCTGGGCTCCA 954
961 TACTGTCTGTTTCAAAATGCTTCAACTTAACTTACCCAGAAAGGAAAGCCCAAAATCGGTG 1020
955 TATTCTCTGTTCAAAATGCTTCAATTTATTCCTCAGCAACAGGTCTCAATCAGTT 1014
1021 TGGTACAGCAATGCTGCTGCTGCAATGTTTCAATTCGTTTGTAAATCCCTTCTGCTAC 1080
1015 TGGTATAGAATGCAATTTGGCTTCAAGTGTCTTCAATTCCTTGTCAATCTCTTTTGTAT 1074
1081 CCTTTGTTGACAGGCGTTTCCAGAGGCTTCTGGAAGATACCTTGTGTGACAAAGCAA 1140
1075 CCATTGTTGACAGGCGCTTCCAAAGGCTTCTTGAAGATATTTTGTATATAAAGCAA 1134
1141 CCAGCGCTGTACAGAAC---CAGTCAAGTATCTTCTGA 1176
1135 CCTTACCATCACACACAGTGGTCAAGTATCTCTTAA 1173
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RESULT 13

US-10-354-769-1

; Sequence 1, Application US/10354769

; Publication No. US20030149242A1

; GENERAL INFORMATION:

```
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-354-769-1
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Query Match 58.4%; Score 686.6; DB 7; Length 1173;

Best Local Similarity 75.1%; Pred. No. 4.7e-205;

Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;

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Qy 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420
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Qy 481 ACGAACACAAGGACTCTGAGCCTGGCTTGTTCAGAGTGGTACATCCTCACCAATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTATACATCCTTGGCCATCACA 534
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Db 661 ACCTCTTCCAGTGTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT 720
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Db 715 TCTGATCGACAGAGTTCTTGATCTTCAATTCAGAGAGACAGAGGAGAAAGATAGT 774
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Db 775 CTATGTTTCTCAAGAACCAAGATGAATAGCAATCAATTTCTTCAAAATGGGTTC 834
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Db 1135 CCTTACCATCACACACAGTCGGTCAATCTTCTTAA 1173

RESULT 14

US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13
Query Match 58.4%; Score 686.6; DB 7; Length 1173;
Best Local Similarity 75.1%; Pred. No. 4.7e-205;
Matches 886; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Qy 1 ATCTCGAGTCTAAACAGTACTGGCATCTTGGCCACACAGCTGCTCAGGTCCCTTTGGCATTT 60
Db 1 ATCCGAGATCTAATAGCAATCAATTTATCAATAGCACTCGTGTACTTTAGCATTT 60
Qy 61 TTAATGCTTCATTTGCCCTTTGCTATAATAGTAGGCAATGCTGTGTCATCTTAGCCTTT 120
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Db 595 TGGAGCTGTGGAAGCTGTGATCATCTCAGTAGTGGCCAAAGCCATCTTGGACTGACTGCT 654
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Db 715 TCTGCACTCGACAGAGATTTCTGTCATCTTTTCAATTCAGAGAGACAGAGAGAGTAGT 774
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Db 775 CTATGTTTCTTCAAGAACCAAGATGAATAGCAATACATTTGTTTCCAAATAGGGTTC 834
Qy 841 TTCTGGCGATCGGAAAGTGCAGGCTTTCGCCAAAGGAGTACGACAGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATCTCTGTAGCTTTCACCAAGGGAACATGTTGAATCTGTAGAGCC 894
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Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTCTTAGGGGTTTTTGTGTTTCTGGGCTCCA 954
Qy 961 TACTGTCTGTTCACAAATTTGCTCTTCAACTTACCCAGAAACGAAACGCTTCAAAATCGGTG 1020

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Qy	1021	TGGTACAGCAATGCCCTTCGGCTGCAATGGTCAATTCGTTTGTATCCCTTTCGTAC	1080
Db	1015	TGGTATAGAAATTGCAATTTGGCTTCAGTGGTCAATTCCTTTGTCAATCCTCTTTTGTAT	1074
Qy	1081	CCTTTGTTGTCACAGGCGTTTCCAGAAAGCCTTCTGGAAGATACCTTTGTGTGACAAAGCAA	1140
Db	1075	CCATTGTGTACAAAGCGCTTTCAAAAGCGCTTCTTGAAAAATATTTGTATATAAAAGCAA	1134
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Db	1135	CCTCTACCATCAACAACAGTCGGTCAGTATCTTCITAA	1173

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RESULT 15
US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
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; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Query Match          58.4%;   Score 686.6;   DB 7;   Length 1173;
Best Local Similarity 75.1%;   Pred No. 4.7e-205;
Matches 886;   Conservative 0;   Mismatches 284;   Indels 9;   Gaps 2;

QY      1   ATGTCGGAGTCTAACAGTACTGGCATCTTCCCAACCACTGCTCAGGTCCTTGGCAATTT 60
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      1   ATGCCAGATACTAATAGCACAAATCTTATCACTAAGCACTCGTGTACTTTTAGCATTT 60

QY      61   TTAATGCTTCATTGCTCTTTTGGCTATTAATCGTAGGCAATGCTGTGGTCATCTTAGCCTTT 120
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      61   TTTATGCTCTTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGGTCATCTTAGCCTTT 120

QY      121  GTGGTGACAGAAACCTTAGACATCGAAGTAATTAATTTTTTCTTAATTTGGCTATTTCT 180

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Search completed: May 22, 2006, 21:38:47

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Job time : 1526 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 21:30:28 ; Search time 24 Seconds
(without alignments)
3457.240 Million cell updates/sec

Title: US-10-626-445-5

Perfect score: 1176

Sequence: 1 atgtcggagttaacagctac.....accagtcagtattcttga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /EMC Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	685	58.2	1265	7	US-11-242-505A-25
3	49.2	4.2	1847	6	US-10-511-937-2881
4	37.4	3.2	1105	7	US-11-312-958-23
5	35.2	3.0	1323	7	US-11-302-678-42
6	35.2	3.0	1984	7	US-11-302-678-40
7	35	3.0	50000	6	US-10-528-659-2
8	34.2	2.9	394191	6	US-10-506-549-3
9	34	2.9	2634	7	US-11-217-529-79043
10	33.8	2.9	5193	7	US-11-317-983-3
11	33.8	2.9	5339	7	US-11-317-983-24
12	33.6	2.9	1143	7	US-11-302-678-21
13	33.6	2.9	1182	7	US-11-302-678-19
14	33.4	2.8	300	7	US-11-217-529-81301
15	33.4	2.8	1074	7	US-11-302-678-39
16	33.4	2.8	1159	7	US-11-302-678-37
17	33	2.8	471	7	US-11-217-529-77805
18	33	2.8	2230	6	US-10-511-937-354
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23	31.8	2.7	1679	6	US-10-473-173-65
24	31.8	2.7	1679	6	US-10-505-928-746
25	31.8	2.7	1679	6	US-10-511-937-428

ALIGNMENTS

RESULT 1

US-11-242-505A-26

; Sequence 26, Application US/11242505A

; Publication No. US2006009656A1

; GENERAL INFORMATION:

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; TITLE OF INVENTION: Methods and Compositions for Treating

; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,

; FILE REFERENCE: MPI2001-288P/RCPLONM

; CURRENT APPLICATION NUMBER: US/11/242,505A

; CURRENT FILING DATE: 2005-10-03

; PRIOR APPLICATION NUMBER: US 10/290,078

; PRIOR FILING DATE: 2002-11-07

; PRIOR APPLICATION NUMBER: US 60/347,949

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 10/320,351

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: 60/341,606

; PRIOR FILING DATE: 2001-12-17

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 26

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1173)

US-11-242-505A-26

Query Match 58.2%; Score 685; DB 7; Length 1173;

Best Local Similarity 75.1%; Pred No. 2,9e-209;

Matches 885; Conservative 0; Mismatches 285; Indels 9; Gaps 2;

QY 1 ATGTGGAGTCTAACAGTACTGGCATCTTGGCCACGAGTGTCTAGCTCCCTTGGCATTT 60

DB 1 ATGCCAGATCTAATAGCAATCAATTTATCACTAAGCACCTCGTTTACTTTAGCATTT 60

QY 61 TTAATGCTTTCATTTGCCCTTTTGTCTATATGTTAGGCAATGCTGTGTCATCTTAGCCTTT 120

DB 61 TTTATGCTTTCATTTAGTCTTTTGTCTATATGTTAGGCAATGCTGTGTCATCTTTAGCCTTT 120

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DB 121 GTGTGGACAAACCTTAGACATCGAAGTAAATTTTTTCTTAATTTTGGCTATTTCT 180

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477 --TGAAGGTAGTGAATGTGAACCTGATTTTTCGGAATGTGATCATCTTCCCATCACA 534
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1141 CCAGCGCTGTACAGAAC --- CAGTCAATCTCTTTGA 1176
1135 CTTCTACCATCACAAACAGTCCGTGCTAGTATCTTCTTAA 1173

RESULT 2
US-11-242-505A-25
; Sequence 25, Application US/11242505A
; Publication No. US2006009965A1

GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P/RCPLONNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-242-505A-25

Query Match 58.2%; Score 685; DB 7; Length 1265;
Best Local Similarity 75.1%; Pred. No. 3.1e-209; Indels 9; Gaps 2;
Matches 885; Conservative 0; Mismatches 285;

QY 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACACAGCTGCTCAGGTCCCTTTGGCATTT 60
DB 55 ATGCCAGATCTAATAGCACATCAATTTATCATAAGCACCTGCTTACTTTAGCATTT 114
QY 61 TTAATGTCCTTCAATTTGCCCTTCTATAATAGTGAAGCAATGCTGTGCTCATCTTTAGCCTTT 120
DB 115 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCACTTTTAGCTTTT 174
QY 121 GTGTGGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAAATTTGGCTATTTCT 180
DB 175 GTGTGGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAACTTTGGCATCTCT 234
QY 181 GACTTCTCTGGGTTTGATTTTCCATTTCTGTATACCTCCCTCAGCTGTTGTTTAACTGG 240
DB 235 GACTTCTTTGGGTGTGATCTCCATTTCTTGTATACCTCCCTCAGCGTGTTCGAATGG 294
QY 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCACTACTGATCTATCTTTTGTGCAACGCA 300
DB 295 GATTTTGGAAAGGAAATCTGTATTTGGCTCACTACTGACTATCTGTATGTACAGCA 354
QY 301 TCTGTCTACAATATTTGCTCTCATCTAGTACGATCCAGTCAGTTCCTCAAAATGCTGTG 360
DB 355 TCTGTATATAACATTTGCTCTCATGATGATCGATACCTGTCACTCAAAATGCTGTG 414
QY 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTTGTTGCTCAAAATGGTGGCTGTTGG 420
DB 415 TCTTATAGAATCTCAACATCTAGTGGGCTTGAAGATTTGTTACTCTGATGTTGTTGGT 474
QY 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTTCTGGCTTCAGATTTCTTGGGAAGACAGC 480
DB 475 GTGCTGGCTTCTTAGTGAATGGGCCAAATGATTTCTAGTTTTCAGAGTCTTGGGAAGGA --- 530
QY 481 ACGAACACAAAGGACTGTGAGCGCTGTTTGTACAGAGTGTGATACCTCCTCACCATTACA 540
DB 531 --TGAAGGTAGTGAATGTGAACCTTGGGATTTTTCGGAATGGTACATCTTGGCATCACA 588
QY 541 ATGCTCTTGAATTTCTCTGCTTCTCTGTCTCATCTCTGTGGCTTTATTTCAATGTACAGATTTAC 600
DB 589 TCATCTTGGAAATTCGTGATCCCGAGTCACTTAGTCTGCTTATTTTCAACATGAATATTTAT 648
QY 601 TGGAGCTGTGGAAGCGCTAGGGCTCTCAGTAGGGTCCCTAGCCATGCTGGATTTCTCCACT 660
DB 649 TGGAGCTGTGGAAGCGCTAGTCTCTCAGTAGGTGCCAAAGCCATCTCTGGGACTGACTCT 708

661	Qy	ACCTCTTCAGTGTTCAGGACACTTACAGAGCTGGGGTGGCTTGACGACAAAGTAAT	720
709	Db	GTCTCTTCCAACTCTGTGGACACTCAATTCAGAGTAGACTATCTTCAAGAGAGATCTCTT	768
721	Qy	CCTGGATTGAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCGNAGAAAGCAGC	780
769	Db	TCTGCATCGACAGAAGTCTCTGCACTCTTCAATTCAGAGAGACGGAGGAGAAAGTAGT	828
781	Qy	ATCCTGCTGTCTTTAAGGACTCACATGAACACGAGTATCACTGCGCTTCAAAAGTGGGTCC	840
829	Db	CTCATGTTTCTCTCAAGAACCAAGATGAATAGCAATCAATGCTTCCAAATGGGTCC	888
841	Qy	TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC	900
889	Db	TTCTCCCAATCAGATTCTGTAGTCTTACCACAAAGGGAAATGTTTGAATGCTTTAGAGCC	948
901	Qy	AGNAGCTAGGCAGGTCACTGGCCATCGTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA	960
949	Db	AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTTGCTGTTTGTCTGGGCTCCA	1008
961	Qy	TACTGCTGTTCACAAATGTGCTTTCAACTTACCCTCAGACGGAAACGCCCAATCGGTG	1020
1009	Db	TATTCTCTGTTCACAAATGTGCTTTTCATTTATTCTCAGCAACAGGCTCTAAATCAGTT	1068
1021	Qy	TGGTACAGCATTTGCTTTCTGGCTGCAATGGTTGCAATTCGTTTGTAATCCCTTTCTGTAC	1080
1069	Db	TGGTATAGAATTGGATTTTGGCTTCAGTGGTTCAATTCCTTTTGCAATCCCTTTTGAT	1128
1081	Qy	CCTTTGTGTCCAGGCGTTTTCCAGAAAGCTTTCTGGAAGATACCTTTGTGACAAAGCAA	1140
1129	Db	CCATTGTGTCCAAAGCGCTTCCAAAGGCTTTCTTGAAATATATTTTGTATATAAAAAAGCAA	1188
1141	Qy	CCAGCGCTGTACAAAC---CAGTCAGTATCTTCTTGA	1176
1189	Db	CTCTACCATCACAAACAGTCGGTCAAGTATCTTCTTAA	1227

RESULT 3

```

RESULT 3
US-10-511-937-2881
/ Sequence 2881, Application US/10511937
/ Publication No. US20060088836A1
/ GENERAL INFORMATION:
/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.
/ APPLICANT: Wohlgemuth, Jay
/ APPLICANT: Fry, Kirk
/ APPLICANT: Woodward, Robert
/ APPLICANT: Ly, Ngoc
/ APPLICANT: Prentice, James
/ APPLICANT: Morris, Macdonald
/ APPLICANT: Rosenberg, Steven
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
/ FILE REFERENCE: 506612000104
/ CURRENT APPLICATION NUMBER: US/10/511,937
/ CURRENT FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/012946
/ PRIOR FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 10/131,831
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 10/325,999
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 3117
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2881
/ LENGTH: 1847
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-511-937-2881

```

Query Match 4.2%; Score 49.2; DB 6; Length 1847;
Best Local Similarity 51.9%; Pred. NO. 4.5e-06;
Matches 136; Conservative 0; Mismatches 123; Indels 3

```

QY 89 TGGTAGGCAATGCTGTGTCACTTTAGCCTTTTGTGGTGGACAGAAACCTTTAGACATCGAA 14
Db 623 TTGCTGGCAATGTGTGTCTGTCTGTGGCGGTGTGAACCGCGGCTCCGCAACCTGA 682
QY 149 GTAATATTATTTTCTTAATTTGGCTATTCTTGACTTCTCGTGGGTTTGATTTCCATTC 208
Db 683 CCAATTTGTTTCATGTGTCTTGGCTATCACTGACCTGTCTCTCGGCTTCTGTGTGCTGC 742
QY 209 CTCTGT---ACATCCCTCACGTGTTGTTTAACTGGAAATTTTGGAAAGTGGAAATCTGCATGT 265
Db 743 CTTTCTCTGCCATCTACACAGCTGTCTCTCAAGTGGAGCTTTTGGCAAGGTCTTCTTGCATA 802
QY 266 TTTGGCTCAATTACTGACTATCTTTTGTGTCACGGCATCTGTCTACAATATTGTCTCTCATTA 325
Db 803 TCTACACAGCCTGGATGTGATGCTCTGCACAGCCTCCATCTTAACTCTTTTCATGATCA 862
QY 326 GCTACGATCGATACCAAGTCAGT 347
Db 863 GCCTGACCGGTACTGCGCTGT 884

RESULT 4
US-11-312-958-23
; Sequence 23, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 625
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 63112, 2158, 224, 615, 44373
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55034, 16314, 1613, 1675, 9
; TITLE OF INVENTION: 13434 MOLECULES
; FILE REFERENCE: MPI02-027P1RNNMIM
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1105
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(1101)
US-11-312-958-23

```

Query Match 3.2%; Score 37.4; DB 7; Length 1105;
Best Local Similarity 53.0%; Pred. No. 0.019;
Matches 80; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 89 TGGTAGCAATGCTGGTGCATCTTAGCCCTTTGTGGTGACAGAAACCTTAGACATCGAA 148
Db 176 TCGTGGCAACCTCCTGGTGAATCTCTCCGTGCTCAGAAACCGAAGCTCCGGAACGCAG 235
QY 149 GTAATATTTTCTTTAAATTTGGCTATTTCTGACATTCCTCGTGGGTTTGATTTCCATTC 208
Db 236 GTAATTTGTTCTTGGTGAGTCTGGCATTTGGCTGACCTGGTGGTGGCTTCTACCCCTACC 295
QY 209 CTCTGATACATCCCTCAGCTGTTGTTAACTG 239
Db 296 CGCTAATCCTCGTGGCCATCTTCTATGACGG 326

RESULT 5

US-11-302-678-42
; Sequence 42, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 42
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1323)
US-11-302-678-42

Query Match 3.0%; Score 35.2; DB 7; Length 1323;
Best Local Similarity 54.8%; Pred. No. 0.11;
Matches 92; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 178 TCTGACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTGTTT 234
Db 211 TCTGACCTGATGGTGGGCTGGTGGTATGCGCGGCCCATGCTGAAACGGCTGTACGGG 270
QY 235 AACTGGAATTTTGAAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGTGC 294
Db 271 CGTGGGTGCTGGCGCGGCCCTCTGCCTGCTCTGGACCGCCCTTCGACGTGATGTGTGC 330
QY 295 ACCGATCTGTCTACAATATTGTCTCATTTAGCTACGATCGATACCAG 342

Query Match 3.0%; Score 35.2; DB 7; Length 1323;
Best Local Similarity 54.8%; Pred. No. 0.11;
Matches 92; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 178 TCTGACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTGTTT 234
Db 211 TCTGACCTGATGGTGGGCTGGTGGTATGCGCGGCCCATGCTGAAACGGCTGTACGGG 270
QY 235 AACTGGAATTTTGAAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGTGC 294
Db 271 CGTGGGTGCTGGCGCGGCCCTCTGCCTGCTCTGGACCGCCCTTCGACGTGATGTGTGC 330
QY 295 ACCGATCTGTCTACAATATTGTCTCATTTAGCTACGATCGATACCAG 342

Db 331 AGCGCCTCCATCTCAACCTCTGCCTCATCAGCCTGACCGCTACCTG 378

RESULT 6

US-11-302-678-40
; Sequence 40, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 40
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (468)...(1790)
US-11-302-678-40

Query Match 3.0%; Score 35.2; DB 7; Length 1984;
Best Local Similarity 54.8%; Pred. No. 0.14;
Matches 92; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 178 TCTGACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGTGTGTGTTT 234
Db 678 TCTGACCTGATGGTGGGCTGGTGGTATGCGCGGCCCATGCTGAAACGGCTGTACGGG 737
QY 235 AACTGGAATTTTGAAGTGAATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGTGC 294
Db 738 CGTGGGTGCTGGCGCGGCCCTCTGCCTGCTCTGGACCGCCCTTCGACGTGATGTGTGC 797
QY 295 ACCGATCTGTCTACAATATTGTCTCATTTAGCTACGATCGATACCAG 342
Db 798 AGCGCCTCCATCTCAACCTCTGCCTCATCAGCCTGACCGCTACCTG 845

RESULT 7

US-10-528-659-2
; Sequence 2, Application US/10528659
; Publication No. US20060099594A1
; GENERAL INFORMATION:
; APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE

APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
APPLICANT: YAMADA, Yoshiji
APPLICANT: YOKOTA, Mitsuhiko
TITLE OF INVENTION: Method for diagnosing a risk of hypertension
FILE REFERENCE: C0200701
CURRENT APPLICATION NUMBER: US/10/528,659
CURRENT FILING DATE: 2005-03-22
PRIOR APPLICATION NUMBER: JP P2002-280034
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 50000
TYPE: DNA
ORGANISM: Homo sapiens
US-10-528-659-2

Query Match 3.0%; Score 35; DB 6; Length 50000;
Best Local Similarity 48.0%; Pred. No. 1.2; Indels 1;
Matches 132; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

Qy 89 TGGTAGGCAATGCTGTGCTCATCTTAGCCCTTTGGTGGACAGAAACCTTAGACATCGAA 148
Db 46275 TTGTGGCAACATGCTGCTCTCATCTTAATAAACTGCAAAAGCTGAAGTCTTGA 46334

Qy 149 GTAATTAATTTTCTTAATTTGCTATTTCTGACTTCTCTCGTGGGTTGATTTCCATTC 208
Db 46335 CTGACATTTACCTGCTCAACCTGCGCATCTCTGATCTGCTTTT--TCTTATTACTCTCC 46391

Qy 209 CTCGTGATATCCCTCAGCTGTGTTTAACTGGAATTTGGAGTGGATCTGCATGTTTT 268
Db 46392 CATTTGGGCTCACTCTGCTGCAAAAGAGTGGGCTTTTGGGAATGCAATGCAAAATAT 46451

Qy 269 GGCTCAATTACTGACTATCTTTTGTGACCGCATCTGCTCAAAATATGCTCTCAATTAGCT 328
Db 46452 TCACAGGCTGATACATCGTTATTTTGGCGGAATCTTCTCATCATCTCTCTGCAA 46511

Qy 329 ACATGATACACATGCTGATTTCAAAATGCTGTCT 363
Db 46512 TCGATAGATACCTGGCTATTGTCATGCTGTGTTT 46546

RESULT 8
US-10-506-549-3
Sequence 3, Application US/10506549
Publication No. US20060100417A1
GENERAL INFORMATION:
APPLICANT: APPLERA CORPORATION
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001361-US
CURRENT APPLICATION NUMBER: US/10/506,549
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/361,343
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 394191
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(394191)
OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match 2.9%; Score 34.2; DB 6; Length 394191;
Best Local Similarity 55.5%; Pred. No. 7.7;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 66 GTCTTCATTTGGCCTTTGCTATTAATGGTAGGCAATGCTGTGCTCATCTTAGCCCTTTGGT 125

Db 62198 GTAATTCCTTCCTTCTGCTAACTCTGAACCTTATTTGTTCTTTTCTATTTCTTTGTTGT 62257
Qy 126 GGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTCTGACT 184
Db 62258 GTAAATATTAGTTGTTCTTCAATTGAGATATTTCTTTTCTTAATATAGTATTATTGCT 62316

RESULT 9
US-11-217-529-79043
Sequence 79043, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 79043
LENGTH: 2634
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-79043

Query Match 2.9%; Score 34; DB 7; Length 2634;
Best Local Similarity 48.9%; Pred. No. 0.4;
Matches 91; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 79 TTGCTATAATGGTAGGCAATGCTGTGTCATCTTAGCCTTTGTTGGTGGACAGAAACCTT 138
Db 1678 TTGCCATATTGATAGGCTCACTTGTGTTGGAATAGCTGTTGTAGAGCACTACCCAACA 1737

Qy 139 AGACATCGAAGTAATTAATTTTCTTAATTTGCTATTTCTGACTTCTCTCGTGGTTTG 198
Db 1738 AATACACCAGTTGGGGCTCTTTTGTGTTAGGATTAATTTGTTCTTCTGATTTCCA 1797

Qy 199 ATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTTAACTGGAATTTGGAAGTGAATC 258
Db 1798 ACTACTATCTTCAAGCAACCACTGGTTTTCGTTTGGTTTGAATCTACTAATTAATG 1857

Qy 259 TGCATG 264
Db 1858 GTGATG 1863

RESULT 10
US-11-317-983-3/c
Sequence 3, Application US/11317983
Publication No. US2006090222A1
GENERAL INFORMATION:
APPLICANT: Zou, Jitao
APPLICANT: Taylor, David C
APPLICANT: Wei, Yangdou
APPLICANT: Jako, Colette C
TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
FILE REFERENCE: 3015-5684.US
CURRENT APPLICATION NUMBER: US/11/317,983
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/11/117,005
PRIOR FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: PCT/CA99/01202
PRIOR FILING DATE: 1999-12-16

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; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5193
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-317-983-3

Query Match      2.9%; Score 33.8; DB 7; Length 5193;
Best Local Similarity 58.4%; Pred. No. 0.72;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 156 TTTTCTTAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215
Db 1355 TTTTCTTAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215

Qy 216 CATCCCTCAGCTGTTGTTAACTGGAATTTTGGAAAGTGGAA 256
Db 1295 CTATATTGAGTGTTTTTTAGTGAATATTTTAAGAAGAA 1255

RESULT 11
US-11-317-983-24/c
; Sequence 24, Application US/11317983
; Publication No. US2006009222A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684.1US
; CURRENT APPLICATION NUMBER: US/11/317,983
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 5339
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-317-983-24

Query Match      2.9%; Score 33.8; DB 7; Length 5339;
Best Local Similarity 58.4%; Pred. No. 0.73;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 156 TTTTCTTAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215
Db 1355 TTTTCTTAATTTGGCTATTTCTGACTTCCTCGTGGTTTGATTTCCATTCCTCTGTA 215

Qy 216 CATCCCTCAGCTGTTGTTAACTGGAATTTTGGAAAGTGGAA 256
Db 1295 CTATATTGAGTGTTTTTTAGTGAATATTTTAAGAAGAA 1255

RESULT 12
US-11-302-678-21
; Sequence 21, Application US/11302678
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
```

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; NUMBER OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012PIRNM.OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1143)
US-11-302-678-21

Query Match      2.9%; Score 33.6; DB 7; Length 1143;
Best Local Similarity 45.2%; Pred. No. 0.32;
Matches 123; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 89 TGTAGGCAATGCTGTGTCATCTTAGCCCTTTGFGTGGACAGAACTTAGACATGAA 148
Db 221 TGTGGGCAACTCGCTGTCATGTTCTGTATCATCCGATACACAAAGATGAAGACAGAA 280

Qy 149 GTAATATTTTTTCTTAATTTGGCTATTTCTGATCTCTCGTGGGTTTGATTTCCATTC 208
Db 281 CCAACATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCCCT 340

Qy 209 CTCTGTATATCCCTCAGCTGTGTTTAACTGGAATTTTGGAAAGTGAATCTGCAATGTTTT 268
Db 341 TTAGAGTACGGTCTACTTGTATGAAATCTTGGGCTTTTGGGATGTCTGTGCAAGATAG 400

Qy 269 GGCTCAATTAAGTACTATPCTTTTGTGACCCGATCTGTCTCAATATTTGCTCTCAATAGCT 328
Db 401 TAAATTTCCATTGATTACTACAAACATGTTCCACGACATCTTCACCTTGACCATGATGACG 460

Qy 329 AGATCCGATACAGTCAAGTTTCAAAATGCTGTG 360
Db 461 TGGACCGCTACATTTGCCGTGTGCCACCCCGTG 492

RESULT 13
US-11-302-678-19
; Sequence 19, Application US/11302678
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
```

```

: TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
: TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
: FILE REFERENCE: MPI02-02PIRNM OMNI
: CURRENT APPLICATION NUMBER: US/11/302.678
: CURRENT FILING DATE: 2005-12-14
: PRIOR APPLICATION NUMBER: US/10/345,680
: PRIOR FILING DATE: 2003-01-16
: PRIOR APPLICATION NUMBER: US 60/349,511
: PRIOR FILING DATE: 2002-01-18
: PRIOR APPLICATION NUMBER: US 60/360,500
: PRIOR FILING DATE: 2002-02-28
: PRIOR APPLICATION NUMBER: US 60/365,041
: PRIOR FILING DATE: 2002-03-15
: PRIOR APPLICATION NUMBER: US 60/374,063
: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: US 60/403,468
: PRIOR FILING DATE: 2002-08-14
: PRIOR APPLICATION NUMBER: US 60/414,262
: PRIOR FILING DATE: 2002-09-27
: PRIOR APPLICATION NUMBER: US 60/419,986
: PRIOR FILING DATE: 2002-10-21
: PRIOR APPLICATION NUMBER: US 60/423,809
: PRIOR FILING DATE: 2002-11-05
: PRIOR APPLICATION NUMBER: US 60/429,797
: PRIOR FILING DATE: 2002-11-26
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19
: LENGTH: 1182
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (14)...(1156)
: OS-11-302-678-19

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Query Match	2.9%;	Score 33.6;	DB 7;	Length 1182;
Best Local Similarity	45.2%;	Pred. No. 0.33;		
Matches 123;	Conservative 0;	Mismatches 149;	Indels 0;	Gaps 0
Qy 89	TGGTAGGCAATGCTGTGGTCAATCTTAGCCCTTTGGTGGACAGAAACCTTAGACATCGAA	148		
Db 234	TGGTGGGCAACTCGCTGGTCAATGTTCTGGTATCATCCGATACACAAAGATGAAGACAGCAA	293		
Qy 149	GTAATTATTTTTTCTTAAATTTGGCTATTTCTGACTTCCTCGTGGGTTTGATTTCCATTTC	208		
Db 294	CCAACTTTACATATTTAAACCTGGCTTTGGCAGATGCTTTTAGTTACTACAAACCATGCGCT	353		
Qy 209	CTCTGTACATCCCTCACGTGTGTTTAACTGGAATTTTGGAAAGTGAATCTGCAATGTTTT	268		
Db 354	TTGAGAGTACGGTCTACTTGAAGAATCTCGCCCTTTTGGGGATGTGCTGTGCAAGATAG	413		
Qy 269	GGCTCATTACTGACTATCTTTTGTGCACCGCATCTGCTCAATAATTTGCTCATTAGCT	328		
Db 414	TAATTTCCATTGATTACTACAACATGTTCCACAGATCTTCCACCTTGACCATGATGAGG	473		
Qy 329	ACGATCGATACCACTGACTGTTTCAAATGCTGTG	360		
Db 474	TGGACCGCTACATTGCCGTGTGCGCAACCCCGTG	505		

RESULT 14
US-11-217-529-81301/c
; Sequence 81301, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

```

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81301
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81301

Query Match      2.8%; Score 33.4; DB 7; Length 300;
Best Local Similarity 48.7%; Pred. No. 0.16;
Matches 91; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy      402 TCAAAATGGTGGCTGTTGGATACATGCGTTCCTTGGTAATATGGCCCGCATGATTCGTGGCTTC 461
Db      300 TCATCTGATTCGTTGTTGTAATATGTCGCTCTTTCAATAGCGCCATTTTGTCTCTCTTC 241

Qy      462 AGATCTCTGGAACACAGACGACGAAACAAGGACTGTGAGCCTGGCTTTGTTACAGAGTG 521
Db      240 GAAATCTTCAAGTAAGACTCTCTGTTATTAATAGATAGGATATCAACCCCTACGAGGC 181

Qy      522 GTACATCTCTCACCATTACAAATGCTCTTGGAAATTCCTGCTTCCTGTGTCATCTCTGTGGCTTA 581
Db      180 GACAAATGAGCGCATAAACAATCTTCTTGAAAACCTGACTCTCTTTTCCAACTCTTCCAA 121

Qy      582 TTTCAAT 588
Db      120 ATGCAAT 114

RESULT 15
US-11-302-678-39
; Sequence 39, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 1074

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:31:49 ; Search time 195 Seconds
(without alignments)
916.778 Million cell updates/sec

Title: US-10-626-445-8
Perfect score: 2048
Sequence: 1 MSSNSTGILPPAAQVPLAF.....WKILCVTKWPAISONQSVSS 391

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_8.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*
 - 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2035	99.4	391	5	AAM50565 Mouse his
2	2035	99.4	391	8	ADO29497 Mouse GPC
3	1745	85.2	391	5	AAM50566 Rat hist
4	1370.5	66.9	390	3	AAB02831 Human G p
5	1370.5	66.9	390	3	AAI71297 Human orp
6	1370.5	66.9	390	4	AAB62445 Human GPC
7	1370.5	66.9	390	4	AAG64477 Human G p
8	1370.5	66.9	390	4	AAB73622 Human G p
9	1370.5	66.9	390	5	AAM53050 Human G p
10	1370.5	66.9	390	5	ABP98629 Human his
11	1370.5	66.9	390	5	ABP78276 Amino aci
12	1370.5	66.9	390	5	AAM50564 Human his
13	1370.5	66.9	390	5	AAG66023 Human his
14	1370.5	66.9	390	5	AAT74906 Amino aci
15	1370.5	66.9	390	6	ABG71960 Human G-p
16	1370.5	66.9	390	6	ABU92265 Human G p
17	1370.5	66.9	390	6	ABP81727 Human his
18	1370.5	66.9	390	6	AAE36417 Human H4
19	1370.5	66.9	390	7	ADG98760 Human orp
20	1370.5	66.9	390	7	ADJ26923 Human end
21	1370.5	66.9	390	8	ADG86375 Human end
22	1370.5	66.9	390	8	ADJ88376 Novel hum
23	1370.5	66.9	390	8	ADO05720 Human his

24	1370.5	66.9	390	8	ADO29496	Ado29496 Human GPC
25	1370.5	66.9	390	8	ADP20168	Adp20168 Human G p
26	1370.5	66.9	390	8	ADQ75074	Adq75074 Human G p
27	1370.5	66.9	390	9	ADY86900	Ady86900 Human his
28	1370.5	66.9	391	5	AAM53052	Aam53052 Human G p
29	1370.5	66.9	392	5	AAM53053	Aam53053 Human G p
30	1370.5	66.9	390	4	AAM51410	Aam51410 Human GPR
31	1366.5	66.7	390	6	AAE36416	Aae36416 Human H4
32	1365.5	66.7	390	8	ADG86522	Adg86522 Human end
33	1238	60.4	389	5	AAM50567	Aam50567 Guinea pi
34	1198	58.5	357	6	AAE36415	Aae36415 Human H4
35	1074.5	52.5	336	6	AAE36414	Aae36414 Human H4
36	1064	52.0	649	8	ADU82861	Adu82861 Ligand up
37	729.5	35.6	415	7	RAO29530	Rao29530 Human H3
38	722.5	35.3	445	2	AAW92975	Aaw92975 Human mAC
39	722.5	35.3	445	2	AAI06322	Aai06322 Human G p
40	722.5	35.3	445	2	AAE67830	Aae67830 Human mus
41	722.5	35.3	445	3	AAI92218	Aai92218 Human his
42	722.5	35.3	445	4	AAE30627	Aae30627 A human h
43	722.5	35.3	445	5	ABB79792	Abb79792 Human his
44	722.5	35.3	445	6	ABR43667	AbR43667 Human his
45	722.5	35.3	445	6	ABP57425	Abp57425 Human his

ALIGNMENTS

RESULT 1
AAM50565
ID AAM50565 standard; protein; 391 AA.
XX
AC AAM50565;
XX
DT 18-MAR-2002 (first entry)
XX
DE Mouse histamine H4 receptor.
XX
KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy.
XX
OS Mus musculus.
XX
FN W0200192485-A1.
XX
PD 06-DEC-2001.
XX
PF 22-FEB-2001; 2001WO-US005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX Lovenberg T, Liu C;
XX WPI; 2002-114339/15.
XX N-PSDB; AAI70981.
XX
PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Claim 13; Fig 5B; 92pp; English.
XX
XX The present sequence is that of a mouse histamine receptor of the H4
XX subtype, as predicted from a cDNA clone isolated from a spleen cDNA
XX library. The invention provides mammalian (human, mouse, rat and guinea
XX pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
XX polypeptides (see AAM50564-67). The nucleic acids have been expressed in
XX recombinant host cells that produce active recombinant protein. The
XX pharmacology of known histamine ligands is demonstrated. Mammalian
XX histamine H4 receptor may be used in gene therapy for the treatment of
XX diseases where it is beneficial to elevate mammalian histamine H4

CC receptor activity. Recombinant protein is useful for identifying
CC modulators of the histamine H4 receptor. Such modulators may be useful
CC for diagnosing, treating or preventing asthma, allergy, inflammation,
CC cardiovascular and cerebrovascular disorders, non-insulin dependent
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
CC the neuroendocrine system, stress and spasticity

XX SQ Sequence 391 AA;

Query Match 99.4%; Score 2035; DB 5; Length 391;
Best Local Similarity 99.7%; Pred. No. 8.2e-202;
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVVDNLRHRSNYFFLNLAIS 60
DB 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVVDNLRHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120
DB 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120
QY 121 SYRAQHTGIMKIYVAQVAVVILAFVNGPMLASDSWKNSNTKDCPGFVTEWYILTTIT 180
DB 121 SYRAQHTGIMKIYVAQVAVVILAFVNGPMLASDSWKNSNTKDCPGFVTEWYILTTIT 180
QY 181 MLEFFLLPVTSVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240
DB 181 MLEFFLLPVTSVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240
QY 241 PGLKESAASHSESPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILLRG 300
DB 241 PGLKESAASHSESPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILLRG 300
QY 301 RKLARSAILLSFAICWAPCYCLFTIVLSTYPTERPKSVWYSTAFWLFNFSFVNPFY 360
DB 301 RKLARSAILLSFAICWAPCYCLFTIVLSTYPTERPKSVWYSTAFWLFNFSFVNPFY 360
QY 361 PLCHRRFQKAFKILCVTKVPALSONQSVSS 391
DB 361 PLCHRRFQKAFKILCVTKVPALSONQSVSS 391

RESULT 2

ADO29497

ID ADO29497 standard; protein; 391 AA.

XX AC ADO29497;

XX 29-JUL-2004 (first entry)

XX Mouse GPCR HRH4, SEQ ID NO:599.

G protein-coupled receptor; GPCR; drug screening; diagnosis;
transgenic mouse; neurological disorder; adrenal gland disorder;
colon disorder; intestinal disorder; cardiovascular disorder;
muscular disorder; blood disorder; immune disorder; bone disorder;
joint disorder; metabolic disorder; nutritive disorder; cancer;
kidney disorder; liver disorder; lung disorder; breast disorder;
ovary disorder; uterus disorder; prostate disorder; testis disorder;
skin disorder; stomach disorder; pancreas disorder; spleen disorder;
thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;
cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
dermatological; antitumor; antithyroid; antiallergic; anorectic;
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
murine; receptor.

XX Mus musculus.

XX WO2004040000-A2.

XX 13-MAY-2004.

PD

XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2003; 2002US-0409303P.
PR 03-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MW, Vassiliadis D, Zeng H;
XX WPI; 2004-390329/35.
DR N-PSDB; ADO30257.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 599; 542pp; English.

CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridize to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., osteoarthritis, rheumatoid
CC AIDS); bone and joint disorders (e.g., osteoporosis); metabolic or nutritive disorders (e.g.,
CC arthritis, gout or osteoporosis); metabolic or nutritive deficiency-related
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 391 AA;

Query Match 99.4%; Score 2035; DB 8; Length 391;
Best Local Similarity 99.7%; Pred. No. 8.2e-202;
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVVDNLRHRSNYFFLNLAIS 60
DB 1 MSESNTGILPPAAQVPLAFIMSFAPAIMVGNVILAFVVDNLRHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120
DB 61 DFLVGLISIPLYIPHYLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120
QY 121 SYRAQHTGIMKIYVAQVAVVILAFVNGPMLASDSWKNSNTKDCPGFVTEWYILTTIT 180
DB 121 SYRAQHTGIMKIYVAQVAVVILAFVNGPMLASDSWKNSNTKDCPGFVTEWYILTTIT 180
QY 181 MLEFFLLPVTSVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240
DB 181 MLEFFLLPVTSVAYFNVQIYWSLWKRRALSRCPSHAGFTTSSASGHLHRAGVACTSN 240

Db 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSPHAGSTTSSASGHLHRAGVACRTSN 240
 Qy 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEALLRG 300
 Db 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEALLRG 300
 Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
 Db 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
 Qy 361 PLCHRRPQKAFWKILCVTKWPALSONQSVSS 391
 Db 361 PLCHRRPQKAFWKILCVTKWPALSONQSVSS 391

RESULT 3

AAM50566

ID AAM50566 standard; protein; 391 AA.

XX

AC AAM50566;

XX

DT 18-MAR-2002 (first entry)

DE Rat histamine H4 receptor.

XX

XX Histamine H4 receptor; rat; antiasthmatic; antiallergenic;
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
 KW diagnosis; gene therapy.

XX Rattus rattus.

XX WO200192485-A1.

XX

PD 06-DEC-2001.

XX

PF 22-FEB-2001; 2001WO-US005914.

XX

PR 31-MAY-2000; 2000US-0208260P.

XX

PA (ORTH) ORTHO-MCNEIL PHARM INC.

XX

PI Lovenberg T, Liu C;

XX

DR WPI; 2002-114339/15.

XX

DR N-PSDB; AAI70982.

XX

PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
 PT the proteins, useful in gene therapy for treating diseases where it is
 PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 13; Fig 6A; 92pp; English.

XX

CC The present sequence is that of a rat histamine receptor of the H4
 CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA
 CC library. The invention provides mammalian (human, mouse, rat and guinea
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
 CC recombinant host cells that produce active recombinant protein. The
 CC pharmacology of known histamine ligands is demonstrated. Mammalian
 CC histamine H4 receptor may be used in gene therapy for the treatment of
 CC diseases where it is beneficial to elevate mammalian histamine H4
 CC receptor activity. Recombinant protein is useful for identifying
 CC modulators of the histamine H4 receptor. Such modulators may be useful
 CC for diagnosing, treating or preventing asthma, allergy, inflammation,
 CC cardiovascular and cerebrovascular disorders, non-insulin dependent
 CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
 CC the neuroendocrine system, stress and spasticity

XX Sequence 391 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 85.2%; Score 1745; DB 5; Length 391;

Best Local Similarity 84.9%; Pred. No. 9.6e-172;

Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSESSTGIIIPPAQVPLAFMLMSFAFAIMVGNNAVILAFVVDRLNLRHRSNYFFLNLAIS 60
 Db 1 MSESNGTDVLPFLTAQVPLAFMLMSLAFITGNNAVILAFVADRLNLRHRSNYFFLNLAIS 60
 Qy 61 DFLVGLISILYIPIHVLFNMFSGICMFWLITDYLCTASVYVNIILISYDRYOSVSNV 120
 Db 61 DFFVGVISIPIYIPIHVLFNMFSGICMFWLITDYLCTASVYVNIILISYDRYOSVSNV 120
 Qy 121 SYRAQHTGIMKIIVAQMVAVMILAFVNGPMLASDSWKNSNTKDCBPGFVTEWYILIT 180
 Db 121 RYRAQHTGILKIIVAQMVAVMILAFVNGPMLASDSWKNSNTKDCBPGFVTEWYILIT 180
 Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSPHAGSTTSSASGHLHRAGVACRTSN 240
 Db 181 AFLEFLLPVSLVYFVSQIYWSLWKRGSLSRCPSPHAGFIATSSRGTHSRRTGLACRTSL 240
 Qy 241 PGLKESAAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALRQREYAEALLRG 300
 Db 241 PGLKEPAASHSESPPRKSSILVSLRTHMSSIIAFKVGSPCRSESPVLHQREHVELLRG 300
 Qy 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
 Db 301 RKLARSLAILLSAFACWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINFY 360
 Qy 361 PLCHRRPQKAFWKILCVTKWPALSONQSVSS 391
 Db 361 PLCHRRPQKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 4
 AAB02831
 ID AAB02831 standard; protein; 390 AA.
 XX
 AC AAB02831;
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.
 XX
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KW identification; agonist; screening; therapeutic; pharmaceutical; mutant.
 XX Homo sapiens.
 OS
 XX WO200022131-A2.
 PN
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US024065.
 XX
 PR 13-OCT-1998; 98US-00170496.
 PR 12-NOV-1998; 98US-0108029P.
 PR 20-NOV-1998; 98US-0109213P.
 PR 16-FEB-1999; 98US-0110060P.
 PR 26-FEB-1999; 99US-0120416P.
 PR 12-MAR-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123944P.
 PR 12-MAR-1999; 99US-0123945P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123948P.
 PR 12-MAR-1999; 99US-0123949P.
 PR 28-MAY-1999; 99US-0136436P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.
 PR 28-MAY-1999; 99US-0137127P.
 PR 28-MAY-1999; 99US-0137131P.
 PR 28-MAY-1999; 99US-0137567P.
 PR 29-JUN-1999; 99US-0141448P.
 PR 27-AUG-1999; 99US-0151114P.
 PR 03-SEP-1999; 99US-0152524P.
 PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.
PR 29-SEP-1999; 99US-0156634P.
PR 29-SEP-1999; 99US-0156653P.
PR 01-OCT-1999; 99US-0157280P.
PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.

XX (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

XX WPI; 2000-317986/27.

DR N-PSDB; AAA46023.

XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.

XX Example 1; Page 89-90; 187pp; English.

XX The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptors agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention

XX Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 3; Length 390;

Best Local Similarity 68.1%; Pred. No. 6.5e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESSTGILPPAAQVPLAFMLSFAPIMGVNAVILAFVVDRLNRHSNYFFFLNLAIS 60

Db 1 MPDNTSTINLSLSTRVTLAPFFMSLVAFALMGNALVILAFVVDKRLNRHSNYFFFLNLAIS 60

QY 61 DFLVGLISLPLYIPLVFNWFGSGICMFLLITDYLLCTASVNIYVLSYDRYQSVNAV 120

Db 61 DFFVGVISLPLYIPLTFLFEWDFGKEICVFLLATDYLLCTASVNIYVLSYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIYAQVAVVAVVILAFVNGPMILASDGMKNSNTKDCPEGFTVEWYILIT 180

Db 121 SYRTQHTGVUKIVLMVAVVAVVILAFVNGPMILVSESKDEGS--EPEPGFSEWYILAIT 178

QY 181 MLLEFLLPVISVAYFNVQIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVARTSN 240

Db 179 SFLEFVIVPVILVAYFNNYVSLWKRDHLSCQSHPLTAVSSNICCHSPRGSLSSRSIL 238

QY 241 PGKESAAHSRSHSPRKSILVSLRTHMNSSTAFKVGSWFSESALRQRYAELLRC 300

Db 239 SASTEPVAPSHSRQRKRSLSMFSSRTKMSNTIASKMGFSQSDSVALLHQREHVELLA 298

QY 301 RKLARSIALLSAFAICWAPCYCLFTVLSYTPRTERPKSVWYSIAFWLQWFNFSVNPFLY 360

Db 299 RLAKSLIALLLGVAVCWAPYSYFTVLSYFSATGPKSVWYIAFWLQWFNFSVNPFLY 358

QY 361 PLCHRRFQKAFWKILCVTKWPAISQ-NQSVSS 391

Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 5

AAAY71297

ID AAY71297 standard; protein; 390 AA.

XX

AC AAY71297;

XX 02-NOV-2000 (first entry)

XX Human orphan G protein-coupled receptor hrUP7.

XX Human; orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;
KW transmembrane receptor; signal cascade.

XX Homo sapiens.

XX WO200031258-A2.

XX 02-JUN-2000.

XX 13-OCT-1999; 99WO-US023687.

XX 20-NOV-1998; 98US-0109213P.

PR 16-FEB-1999; 99US-0120416P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123949P.

PR 28-MAY-1999; 99US-0136436P.

PR 28-MAY-1999; 99US-0136437P.

PR 28-MAY-1999; 99US-0136439P.

PR 28-MAY-1999; 99US-0136567P.

PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.

PR 29-JUN-1999; 99US-0141448P.

PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.

PR 29-SEP-1999; 99US-0156634P.

PR 29-SEP-1999; 99US-0156653P.

PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.

PR 01-OCT-1999; 99US-0157293P.

PR 12-OCT-1999; 99US-0157294P.

PR 12-OCT-1999; 99US-00416760.

PR 12-OCT-1999; 99US-00417044.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Liaw CW, Lin I;

XX WPI; 2000-400068/34.

XX N-PSDB; AAD01124.

XX Novel human orphan G protein-coupled receptors and the encoding cDNAs for
PT use in the identification of G protein-coupled receptor agonists.

XX Claim 26; Page 60-61; 102pp; English.

XX The present amino acid sequence is the hrUP7, an endogenous human orphan
CC G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned
CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
CC GPCR of the invention, like all GPCRs has seven transmembrane alpha
CC helices with an extracellular N-terminus and an intracellular C-terminus.
CC However, no endogenous ligands has yet been identified for the proteins
CC of the invention. The orphan GPCRs may be used in the identification of
CC their endogenous ligands, and to screen potential GPCR agonists and
CC antagonists for use as pharmaceutical agents. The proteins may also be
CC used in the study of GPCR-mediated signalling cascades, and to elucidate
CC their precise role in normal and diseased human conditions. Nucleic acid
CC encoding human orphan GPCRs may be used for tissue localisation
CC expression analysis to provide information about their function in
CC healthy and pathological states

XX Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 3; Length 390;

Best Local Similarity 68.1%; Pred. No. 6.5e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

PF 20-DEC-2000; 2000WO-JF009038.
XX
PR 20-DEC-1999; 99JP-00361687.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Itadani H, Nakamura T, Tanaka K, Ohta M;
XX WPI; 2001-441675/47.
DR N-PSDB; AAH47911.
DR
XX G protein-coupled receptor protein BG26, with activity of binding to
PT histamine and capable of changing intracellular cAMP concentration in
PT response to its stimulus, applicable as tool in screening ligands or drug
PT candidates.
XX
XX Claim 1; Page 41-44; 50pp; Japanese.
PS
XX The present sequence is that of the human G protein-coupled receptor
CC protein BG26, which shows significant homology with histamine H3, with
CC activity of binding to histamine and capable of changing intracellular
CC cAMP concentration in response to its stimulus. The protein is applicable
CC as a tool in screening ligands or drug candidates for regulating signal
CC transduction from such protein and treating diseases associated with its
CC abnormality
XX
SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 6.5e-133;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSENSTGILPPAAQVPLAFMSFAIAIMVGNVILAFVVDNLRHSNRYFLNLAIS 60
Db 1 MPTNSTINLSLSTRTVLAFFMSLVAFIMLGNALVILAFVVDNLRHSNRYFLNLAIS 60

Qy 61 DFLVGLISILPIYIPIHVLNFFNFGSGICMFWLITDYLCTASVNVNIVLSYDRYQSVSNV 120
Db 61 DFFVGVVISIPIYIPIHTLFEWDFGKEICVFWLITDYLCTASVNVNIVLSYDRYLSVSNV 120

Qy 121 SYRAQHTGIMKIVAQVAVMILAFVNGPMILASDSWKNSTNTKDCBPGFVTEWYILIT 180
Db 121 SYRTQHTGLKIVLMVAVVLAFLVNGPMILVSESWKDEGS--ECEPGPFSEWYILAIT 178

Qy 181 MLLEFLPLVTSVAYENVQIVKSLWKRALGRCSHAGFTSTSSASGHLHRAGVACETSN 240
Db 179 SFLEFVPIVLIVAYFNWNIYWSLWKRDHLRCQSHPGLTAVSSNICGHSFRGLSSRRSL 238

Qy 241 PGLKESAAHSSESPRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILLRG 300
Db 239 SASTEVPAFPHSERQQRKSSLMFSRTKMSNTIASKMGFSQSDSVALLQREHVELLRA 298

Qy 301 RKLARSAILLSAFAICWAPCYLFTIVLSYTPRTERPKSVWYISAFWLQWPNFSPVNPFLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWPNFSPVNPFLY 358

Qy 361 PLCHRRFQKAFKWLCLVTWKPALSO-NQSVSS 391
Db 359 PLCHKRFQKAFKIFCIKQPLPSQHSRVS 390

RESULT 8
ID AAB73622 standard; protein; 390 AA.
XX
AC AAB73622;
XX
XX 10-AUG-2001 (first entry)
XX
XX Human G protein-coupled receptor AXOR35.
DE AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW

KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW severe depression; bipolar disorder; depression; delirium; dementia;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery.
XX
XX Homo sapiens.
OS
XX WO200133221-A1.
PN
XX 10-MAY-2001.
PD
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
PR
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;
PI Michalovich D, Morrow DM, Zhu Y;
PI
XX WPI; 2001-316464/33.
DR N-PSDB; AAH24007.
DR
XX Novel G-protein coupled receptor polypeptide and polynucleotide for
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
PT disorders and for identifying modulators useful for treating asthma.
XX
XX Claim 1; Page 50-51; 54pp; English.

CC The invention relates to the human G protein-coupled receptor AXOR35
CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
CC transmembrane domains and is involved in signal transduction. AXOR35 has
CC homology and structural similarity with G protein-coupled receptors such
CC as the human histamine H3 receptor. The invention also relates to
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
CC including bacterial, fungal, protozoal and viral infections, particularly
CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
CC urinary retention; acute heart failure; hypotension; hypertension; angina
CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
CC psychotic and neurological disorders such as anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia, and severe mental
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
CC antibodies may be used in screening compounds for their ability to
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are
CC particularly useful for treating asthma, and inhibiting or promoting the
CC function of lymphocytes, macrophages, eosinophils or neutrophils in
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
CC useful for diagnosing or determining susceptibility of an individual to a
CC disease via the detection of abnormal levels of protein or mRNA, or via
CC the detection of mutations in the corresponding gene. AXOR35 proteins are
CC also useful for inducing an immunological response in a mammal against
CC the above diseases, and for antibody production. AXOR35 nucleotides are
CC also useful as diagnostic reagents, in chromosome localisation and tissue
CC expression studies, and for producing transgenic animals useful in drug
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
CC protein or fragments thereof, and are also useful for treating conditions
CC associated with the expression of the AXOR35 protein. The present
CC sequence represents human AXOR35

```
XX      Sequence 390 AA;
SQ      Query Match      66.9%; Score 1370.5; DB 4; Length 390;
      Best Local Similarity 68.1%; Pred. No. 6.5e-133;
      Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy      1 MSENSTGILPPAAQVPLAFMLSSFAFAIMVGNNAVILAFVVDRLNRHSRYFFLNLAIS 60
Db      1 MPDTNSTINLSLSTRVTTLAFPMSLVAFAIMLGNALVILAFVVDKLNLRHSRYFFLNLAIS 60

Qy      61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLCTASVYNILVLSYDRYOSVSNV 120
Db      61 DFFVGVISIPLYIPHTLFWDFGKEICVFWLTTDYLCTASVYNILVLSYDRYOSVSNV 120

Qy      121 SYRAQHTGIMKIVAQMVWILAFVLNGPMLIASDSWKNSTNKDCPEGFVTEWYILIT 180
Db      121 SYRTQHTGVKIVLWVAVLAFVLNGPMLIVSESWKDEGS--ECEPGFFSEWYILAIT 178

Qy      191 MLLEPLLPIVSIVPNVOIYNSLWKRRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db      179 SFLEFVIPVLVAVFNNMIYNSLWKRRDLRCQSHPGLTAVSSNICGHSFRGLSSRRSL 238

Qy      241 PGLKESARSRSESPRRKSSILVSLRTHMNSITAFKVGSWFSRSESAAALROREYAEILRG 300
Db      239 SASTEVPAFSEHQRRKSSLMFSRTRKNSNTTASRKGWFSQSDSVLHQREHVVELLRA 298

Qy      301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSYAFWLQWNSFVNPLY 360
Db      299 RRLAKSLAILLGPAVCWAPYSLFTIVLSYFSSATGPKSVWYRFAFWLQWNSFVNPLY 358

Qy      361 PLCHRRFOKAFKWLICVTWKPALSQ-NOSVSS 391
Db      359 PLCHKRFOKAFKLFCKIKKQLPSQHSRSVSS 390

RESULT 9
AAM53050
ID      AAM53050 standard; protein; 390 AA.
AC
XX
AC      AAM53050;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Human G protein-coupled receptor nGPCR-2067.
XX
KW      Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;
KW      signal transduction; mental disorder; central nervous system disease;
KW      metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;
KW      psychotic disorder; Huntington's disease; schizophrenia; migraine;
KW      depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;
KW      Parkinson's disease; proliferative disorder; cancer; psoriasis;
KW      benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;
KW      thyroid disorder; cardiovascular disease; hypotension; hypertension;
KW      thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
KW      inflammatory conditions; autoimmune disorder; rheumatoid arthritis;
KW      hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
KW      antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;
KW      cardiant; antiatherosclerotic; neuroleptic; antimigraine;
KW      antiparkinsonian; tranquiliser; antidepressant; neuroprotective;
KW      anticonvulsant; antiinflammatory; antirheumatic; antiarthritic;
KW      antipsoriatic; gene therapy; receptor.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      Domain      19..41
FT      FT      /label= Transmembrane_domain_1
FT      Domain      52..74
FT      FT      /label= Transmembrane_domain_2
FT      Domain      86..110
FT      FT      /label= Transmembrane_domain_3
FT      Domain      128..146
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FT      Domain      /label= Transmembrane_domain_4
FT      FT      172..194
FT      Domain      /label= Transmembrane_domain_5
FT      FT      305..326
FT      Domain      /label= Transmembrane_domain_6
FT      FT      342..360
FT      FT      /label= Transmembrane_domain_7
XX      WO200185793-A2.
PN      15-NOV-2001.
PD
XX      08-MAY-2001; 2001WO-US014750.
PF
XX      08-MAY-2000; 2000US-0203108P.
PR      (PHAA ) PHARMACIA & UPJOHN CO.
PA
XX      Lind P, Sejltitz T, Vogeli G, Wood LS;
XX      WPI; 2002-062240/08.
DR      N-PSDB; ABA02496.
XX
XX      New polynucleotide, useful for identifying modulator compounds which are
XX      used for treating psoriasis, schizophrenia, diabetes, encodes the novel G
XX      protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067)).
XX      Claim 31; Page 63; 100pp; English.
XX
XX      This sequence represents a novel human G protein-coupled receptor (GPCR)
XX      designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative
XX      transmembrane domains and is involved in signal transduction. The
XX      invention also relates to expression vectors and host cells comprising
XX      nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-
XX      2067, to antibodies specific for nGPCR-2067, to drug screening methods
XX      that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067
XX      nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants
XX      and species homologues and may also be used in genetic mapping. The
XX      invention also discloses the use of nGPCR-2067 nucleic acids in screening
XX      for a predisposition to nGPCR-2067-associated hereditary mental
XX      disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic
XX      acids may additionally be used to generate transgenic animals, including
XX      knockout animals, which may provide an insight into treating a variety of
XX      human disorders, and may also be used in the design of antisense
XX      molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067,
XX      and nGPCR-2067 modulators may be used to treat a wide variety of medical
XX      conditions, particularly mental disorders. Diseases that may be treated include
XX      diseases, and metabolic diseases. Diseases that may be treated include
XX      viral infections, particularly HIV-1 or HIV-2 infections; pain; central
XX      nervous system, neurological and psychotic disorders such as Huntington's
XX      disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,
XX      dementia, Alzheimer's disease, and Parkinson's disease; proliferative
XX      disorders such as cancers, benign prostatic hypertrophy and psoriasis;
XX      metabolic disorders such as diabetes, dyslipidaemia, obesity, and
XX      anorexia; thyroid disorders; cardiovascular diseases such as hypotension,
XX      hypertension, thrombosis, myocardial infarction, cardiomyopathies, and
XX      atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,
XX      rheumatoid arthritis); hormonal disorders; and renal failure
XX
SQ      Sequence 390 AA;
      Query Match      66.9%; Score 1370.5; DB 5; Length 390;
      Best Local Similarity 68.1%; Pred. No. 6.5e-133;
      Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy      1 MSENSTGILPPAAQVPLAFMLSSFAFAIMVGNNAVILAFVVDRLNRHSRYFFLNLAIS 60
Db      1 MPDTNSTINLSLSTRVTTLAFPMSLVAFAIMLGNALVILAFVVDKLNLRHSRYFFLNLAIS 60

Qy      61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLCTASVYNILVLSYDRYOSVSNV 120
Db      61 DFFVGVISIPLYIPHTLFWDFGKEICVFWLTTDYLCTASVYNILVLSYDRYOSVSNV 120
```


XX Behan JX, Hedrick JA, Laz TW, Monsma FJ, Morse KL, Umland SP;
PI Wang S;
XX
XX WPI; 2002-673827/72.
XX N-PSDB; ABW78739.
XX
XX Novel mammalian histamine receptor polypeptide useful for identifying
PT agonist or antagonist for treating diseases such as inflammation, asthma,
PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
XX
XX Claim 2; Page 16-17; 21pp; English.
XX
XX The present sequence represents a histamine receptor. The polypeptide is
CC useful for identifying an agonist or antagonist of a mammalian histamine
CC receptor. It is useful as an antigen to elicit the production of
CC antibodies. The histamine receptor polypeptide and polynucleotide are
CC useful in the treatment and management of diseases such as inflammation,
CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,
CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid
CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.
CC They are also useful for modulating intracellular second messenger
CC pathway activated through histamine receptors (cyclic-AMP, calcium,
CC inositol phosphate and mitogen activated protein (MAP) kinase), changes
CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca²⁺
CC mobilization, mitogenic effects, etc
XX
XX Sequence 390 AA;
XX
XX Query Match 66.9%; Score 1370.5; DB 5; Length 390;
XX Best Local Similarity 68.1%; Pred. No. 6.5e-133;
XX Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
XX
QY 1 MSENSTGILPPAAQVPLAFMLSSFAFAMVGNVILAFVVDRLRHRSYFFLNLAIS 60
DB 1 MPDNTNSTINLSRVTPLAFMSLVAFAMLGNAVLILAFVVDKRLRHRSYFFLNLAIS 60
QY 61 DFLVGLISILPIYIPHLFNNFGSGICMFWLITDYLCTASVYNIIVLISYDRYOSVNAV 120
DB 61 DFFVGVISILPIYIPHTLFEWDFGKEICVFWLTDTLLCTASVYNIIVLISYDRYOSVNAV 120
QY 121 SYRAQHTGIMKIIVAQVAVVILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180
DB 121 SYRTQHTGVLKIVTLVAVVVLAFVNGPMLVSESWKDEGS--ECEPGGFSEWYILAIT 178
QY 181 MLLEFLPVISVAYFNVQIYWSLWKRALSRCPHAGFTTSSASGHLRHAGVACRTSN 240
DB 179 SFLEFVIVILVAYFNNIYWSLWKRDHLRCQSHPGLTAVSSNICGHSFGRLSRRSL 238
QY 241 PGLKESAAHRSHSPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILRG 300
DB 239 SASTEVPAFPHSERQRKSSLMFSSRTKMSNTTASRWGFSQSDSVALLHQREHVELLA 298
QY 301 RKLARSLAILLSAPAIQWAPYCLFTIVLSTYPRTERPKSVWYISAFWLQFNFSFVNPFLY 360
DB 299 RRLAKSLAILLGVPAVCWAPYSLFTIVLSFYSSATGPKSVWYIRAFWLQFNFSFVNPFLY 358
QY 361 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 391
DB 359 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 390
RESULT 12
AAM50564
ID AAM50564 standard; protein; 390 AA.
XX
XX AAM50564;
XX
XX 18-MAR-2002 (first entry)
XX
XX Human histamine H4 receptor.
XX
XX Histamine H4 receptor; human; antiasthmatic; antiallergenic;

KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy.
XX
XX Homo sapiens.
XX W0200192485-A1.
XX
XX 06-DEC-2001.
XX
XX 22-FEB-2001; 2001WO-US005914.
XX
XX 31-MAY-2000; 2000US-0208260P.
XX
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX Lovenberg T, Liu C;
XX
XX WPI; 2002-114339/15.
XX N-PSDB; AAI70980.
XX
XX New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX Claim 13; Fig 2; 92pp; English.
XX
XX The present sequence is that of a human histamine receptor of the H4
CC subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA
CC library. The invention provides mammalian (human, mouse, rat and guinea
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC recombinant host cells that produce active recombinant protein. The
CC pharmacology of known histamine ligands is demonstrated. Mammalian
CC histamine H4 receptor may be used in gene therapy for the treatment of
CC diseases where it is beneficial to elevate mammalian histamine H4
CC receptor activity. Recombinant protein is useful for identifying
CC modulators of the human histamine H4 receptor. Such modulators may be
CC useful for diagnosing, treating or preventing asthma, allergy,
CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin
CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
CC disorders of the neuroendocrine system, stress and spasticity
XX
XX Sequence 390 AA;
XX
XX Query Match 66.9%; Score 1370.5; DB 5; Length 390;
XX Best Local Similarity 68.1%; Pred. No. 6.5e-133;
XX Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;
XX
QY 1 MSENSTGILPPAAQVPLAFMLSSFAFAMVGNVILAFVVDRLRHRSYFFLNLAIS 60
DB 1 MPDNTNSTINLSRVTPLAFMSLVAFAMLGNAVLILAFVVDKRLRHRSYFFLNLAIS 60
QY 61 DFLVGLISILPIYIPHLFNNFGSGICMFWLITDYLCTASVYNIIVLISYDRYOSVNAV 120
DB 61 DFFVGVISILPIYIPHTLFEWDFGKEICVFWLTDTLLCTASVYNIIVLISYDRYOSVNAV 120
QY 121 SYRAQHTGIMKIIVAQVAVVILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180
DB 121 SYRTQHTGVLKIVTLVAVVVLAFVNGPMLVSESWKDEGS--ECEPGGFSEWYILAIT 178
QY 181 MLLEFLPVISVAYFNVQIYWSLWKRALSRCPHAGFTTSSASGHLRHAGVACRTSN 240
DB 179 SFLEFVIVILVAYFNNIYWSLWKRDHLRCQSHPGLTAVSSNICGHSFGRLSRRSL 238
QY 241 PGLKESAAHRSHSPRRKSSILVSLRTHMNSSITAFKVGFWRSSESAALRQREYAEILRG 300
DB 239 SASTEVPAFPHSERQRKSSLMFSSRTKMSNTTASRWGFSQSDSVALLHQREHVELLA 298
QY 301 RKLARSLAILLSAPAIQWAPYCLFTIVLSTYPRTERPKSVWYISAFWLQFNFSFVNPFLY 360
DB 299 RRLAKSLAILLGVPAVCWAPYSLFTIVLSFYSSATGPKSVWYIRAFWLQFNFSFVNPFLY 358
QY 361 PLCHRRFQKAFKILCVTKWPALSQ-NQSVSS 391

||||:||||| |||:| | | | | :|||
 359 PLCHRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 13

AAAG66023
 ID AAG66023 standard; protein; 390 AA.

XX AC AAG66023;

XX DT 27-FEB-2002 (first entry)

XX Human histamine H4 receptor protein.

XX Histamine receptor; H4; anti-rheumatic; antiarthritic; immunosuppressive;
 KW antiaesthetic; antiallergic; neuroprotective; antidiabetic; human;
 KW cerebroprotective; cAMP modulator; gene therapy.

XX OS Homo sapiens.

Key	Location/Qualifiers
Domain	12..40
FT	/note= "transmembrane domain"
Domain	52..69
FT	/note= "transmembrane domain"
Domain	88..110
FT	/note= "transmembrane domain"
Domain	130..154
FT	/note= "transmembrane domain"
Domain	172..196
FT	/note= "transmembrane domain"
Domain	304..325
FT	/note= "transmembrane domain"
Domain	342..362
FT	/note= "transmembrane domain"

XX WO200185786-A2.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US014527.

XX 05-MAY-2000; 2000US-0202151P.

XX 23-AUG-2000; 2000US-0227567P.

XX 13-NOV-2000; 2000US-0247855P.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Jones PG, Blatcher M, Wu S, Pausch MH;

XX WPI; 2002-049442/06.

XX N-PSDB; AAI67750.

XX New histamine receptor, termed H4 useful for detecting H4 (ant)agonists

XX for treating transplanted organ rejection, asthma, allergy, multiple

XX sclerosis and rheumatoid arthritis.

XX Claim 5; Fig 1; 66pp; English.

XX The invention provides an isolated histamine receptor, H4, which binds
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
 CC receptor can be expressed by standard recombinant methodology. Cells
 CC expressing H4 receptor protein at a detectable level can suppress cyclic
 CC adenosine monophosphate (cAMP) formation when contacted with the H4
 CC receptor agonist. The H4 receptor and antibodies are used for identifying
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
 CC for treating transplanted organ rejection, asthma, allergies and
 CC autoimmune pathologies such as multiple sclerosis, type I diabetes,
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
 CC protein and nucleic acids are useful targets to identify drugs that are
 CC effective in treating disorders associated with histamine-regulated
 CC processes. Identification and isolation of H4 receptor provides for
 CC development of screening of molecules that interact with H4 receptors.

CC Genetic variants of H4 can be used to diagnose an H4 associated disease
 CC as described above. The H4 receptor polynucleotide is useful to treat or
 CC prevent a disorder associated with the function of H4 in peripheral blood
 CC leukocytes. The present sequence represents the human histamine H4
 CC receptor protein

XX SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;

Best Local Similarity 68.1%; Pred. No. 6.5e-133;

Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNSTGILPPAAQVPLAFMLSSFAFAMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60

DB 1 MPDTNSTINLSLSTRVTLAFPMSLVAFAMLGALVILAFVVDKRLRHSRYFFLNLAIS 60

QY 61 DFVLGLISPLYIPHYLFWNFGSGICMEFWLITDYLLCTASVYNIYLISYDRYQSUSNAV 120

DB 61 DFFVGVISPLYIPTLFEWDFGKEICVFWLTATDYLLCTASVYNIYLISYDRYLSVNAV 120

QY 121 SYRAQHTGIMKIVAQVAVVAVVILAFVNGPMLASDSWKNSTNTKDCPPGFVTEWYILTIT 180

DB 121 SYRTQHTGVLLKIVTLVAVVAVVILAFVNGPMLVSESKDEGS--ECPGFSEWYILAIT 178

QY 181 MLLEFLLPVISVAYFNQIYWSLWKRRLSRCPSHAGFTTSSASGHLRAGVACTSN 240

DB 179 SFLEFVTPVLVAYFNQIYWSLWKRDLHLSRCQSHPLGTAVSSNICGHSFGRLLSSRRSL 238

QY 241 PGLKESAAASHSESPPRKSSILVSLTHMNSSITAFKVSFWSESNAALQREYAEALLRG 300

DB 239 SASTEVPASPHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVVALHQREHVELLRA 298

QY 301 RKLARSLAILLSAPAIQWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLQNFNSFVNPFY 360

DB 299 RRLAKSLAILLGVFVAVCWAPYSFTIVLSFYSSATGPKSVWYIAFWLQNFNSFVNPFY 358

QY 361 PLCHRFQKAFKILCVTKWPALSQ-NQSVSS 391

DB 359 PLCHRFQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 14

AAU74906

ID AAU74906 standard; protein; 390 AA.

XX AC AAU74906;

XX DT 09-APR-2002 (first entry)

XX Amino acid sequence of human G-protein coupled receptor TGR62 protein.

XX Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease;

XX signal transduction modulator; cerebral cavernous malformation;

XX hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;

XX nephritis; hypertension; liver disease; cirrhosis; blood disorder;

XX spleen-associated disorder; immune disorder.

XX OS Homo sapiens.

XX WO200200719-A2.

XX 03-JAN-2002.

XX 25-JUN-2001; 2001WO-US020363.

XX 23-JUN-2000; 2000US-0213461P.

XX (TULA-) TULARIK INC.

XX Lin DC, Zhao J, Chen J, Cutler G;

XX WPI; 2002-147880/19.

XX N-PSDB; ABK12959.

XX New G-protein coupled receptor polypeptides, useful for identifying
PT modulators of signal transduction for treating kidney disease,
PT hyperlipidemia, obesity, dyslexia and cardiac myxoma.
XX
PS Claim 26; Page 61; 78pp; English.
XX
CC The present invention relates to a new G-protein coupled receptor (GPCR)
CC polypeptide comprising greater than 70% amino acid sequence identity to
CC the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2,
CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18 or
CC 90% amino acid sequence identity to human novel edg receptor protein, as
CC defined in the specification. The GPCR covalently linked to a solid phase
CC is useful for identifying a compound that modulates signal transduction.
CC The identified compounds are useful for treating kidney disease, cerebral
CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac
CC myxoma. The molecules of the invention are useful for diagnosing
CC disorders or conditions such as kidney-related conditions or diseases
CC such as renal failure, nephritis, nephrotic syndrome, asymptomatic
CC urinary abnormalities, renal tubule defects, hypertension and
CC nephrolithiasis, liver-related disease or condition e.g. cirrhosis,
CC infiltrations, lesions, functional disorders and jaundice and spleen-
CC associated disorders or conditions e.g. splenic enlargement, immune
CC disorders, blood disorders and others. Modulation of the polypeptide of
CC the invention is useful to treat or prevent any of the above conditions
CC or diseases. The present amino acid sequence represents the human GPCR
CC TGR62 protein of the invention. This sequence is one of seven novel G
CC protein coupled receptors of the invention (AAU74904- AAU74911)
XX
SQ Sequence 390 AA;

Query Match 66.9%; Score 1370.5; DB 5; Length 390;
Best Local Similarity 68.1%; Pred. No. 6.5e-133;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSENSTGILPPAAQVPLAFMLSPFAIMVGNVAVILAFVVDNLRHRSYFFNLAI 60
Db 1 MPDNTNINSLSTRVTLAFPMFLVAFVAFMLGNALVILAFVVDNLRHRSYFFNLAI 60
Qy 61 DFLVGLISIPLYIPHLVFNWFGGICMFWLITDYLCTASVYVNLISYDRYOSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTYLLCTASVYVNLISYDRYLSVNAV 120
Qy 121 SYRAQHTGIMKIVAQVAVVILAFVNGPMLASDMKNSTNTKDCBPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVTLVAVVILAFVNGPMLVSESMKDEGS--ECBPGFSEWYILAIT 178
Qy 181 MLLEFLIPVIVAVFVQVYVSLWKRLSRCPHAGFTTSSASGHLHRAGVACTSN 240
Db 179 SFLEFVIVPILVAVFNNIYVSLWKRDHLRSCQHPGLTAVSSNICGHSFGRLLSRRSL 238
Qy 241 PGLKESAAHRSSEPRKSSITLVSLRTHMNSSITAFKVGSPWRSESAALRQREYAEILRG 300
Db 239 SASTEVPAHSEHQRKRSKLMFSRRTMNSNTTASRKGFSQSDSVALHQREHVELLR 298
Qy 301 RKLARSAILLSAPAIWAPYCLPTIIVLSTYPRTERPKSVWYSIAFWLQFNFSVPNPLY 360
Db 299 RRLAKSLAILLGVAVCWAPVSLFTIVLSFYSSATGPKSVWYRTAFWLFQFNFSVPNPLY 358
Qy 361 PLCHRRFQKAFWKLCTVTKVPALSQ-NOSVSS 391
Db 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRVSS 390

RESULT 15
ABG71960
ID ABG71960 standard; protein; 390 AA.

XX AC ABG71960;
XX
DT 28-JAN-2003 (first entry)
XX
DE Human G-protein coupled receptor AXOR35.

XX Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte;
KW macrophage; eosinophil; neutrophil; infection; transplant rejection;
KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;
KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;
KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;
KW psoriasis; urological disease; urinary retention; cardiovascular disease;
KW myocardial infarction; hypotension; hypertension; pulmonary disorder;
KW chronic obstructive pulmonary disease; cough; renal disease;
KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;
KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;
KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
KW graft versus host disease; osteoporosis.
XX
OS Homo sapiens.
XX
PN US2002137054-A1.
XX
PD 26-SEP-2002.
XX
XX 20-JUL-2001; 2001US-00910411.
XX
XX 02-NOV-1999; 99US-00431898.
XX
XX 03-FEB-2000; 2000US-00497790.
XX
XX 20-OCT-2000; 2000US-00693761.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X;
FI Michalovich D, Morrow DM, Zhu Y;
XX
XX WPI; 2003-074982/07.
XX
XX N-PSDB; ABS57063.
XX
XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for
PT treating infections, gastrointestinal disorders, autoimmune disorders,
PT urological diseases, cardiovascular diseases and cancer.
XX
PS Claim 1; Page 22; 24pp; English.
CC
CC The invention relates to an isolated G-protein coupled receptor
CC polypeptide, AXOR35, (and its homologues and variants) and its encoding
CC polynucleotide (and its homologues, variants, complements and RNA
CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35
CC expression vector, producing a recombinant host cell by introducing the
CC vector into a cell such that the host cell produces AXOR35, a membrane of
CC the host cell expressing AXOR35, identifying/screening for agonists or
CC antagonists of AXOR35 and inhibiting or promoting the function of
CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,
CC by administering to the patient AXOR35 agonists or antagonists. The
CC agonist or antagonist identified is useful for treating a disease such as
CC asthma, or for inhibiting or promoting the function of lymphocytes,
CC macrophages, eosinophils, or neutrophils in diseased tissue such as an
CC atherosclerotic lung. AXOR35 or polynucleotide is useful in diagnostic assays,
CC for identifying compounds that are agonists or antagonists of AXOR35, as
CC vaccines, or for treating infections (bacterial, fungal, protozoan or
CC viral infections), transplant rejection, gastrointestinal disorders (such
CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
CC irritable bowel syndrome, vomiting, inflammation (such as atopic
CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
CC psoriasis), urological diseases (such as urinary retention),
CC cardiovascular diseases (such as myocardial infarction), hypotension,
CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary
CC disease), cough, renal diseases (such as renal ischaemia),
CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders
CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft
CC versus host disease and osteoporosis. The present sequence represents
CC human AXOR35
XX
SQ Sequence 390 AA;

Query Match	66.9%	Score 1370.5	DB 6	Length 390
Best Local Similarity	68.1%	Pred. No. 6.5e-133		
Matches 267	Conservative 40	Mismatches 82	Indels 3	Gaps 2
Qy	1	MSENSGTGLPPAAQVLAFLMSSFAFIMYGVNAWVILAFVVDRLNLRHSRYFFNLNLAIS	60	
Db	1	MPDINSINISLSTRVILAFFMSLVAFAMLCNALVILAFVVDKGLRHSRYFFNLNLAIS	60	
Qy	61	DFLVGLISIPLYIPHLVFNWNGSGICMFWLITYLLCTASVYINVLISYDRYQSVSNV	120	
Db	61	DFFGVVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYINVLISYDRYLSVSNV	120	
Qy	121	SYRAQHTGIMKIQAQMAVAVWILAFLVNGPMLIASDSWKNSNTNKDCPGFVTEVYILIT	180	
Db	121	SYRTQHTGVLKIVLMAVAVWILAFLVNGPMLIVSSEWKEGS--ECSPGPFSEVYILAIT	178	
Qy	181	MLLEFLPLVISVAYFNVIQIYWSLWKRRALSRCPSHAGFSTTSSSAGHLHRAGVACRTSN	240	
Db	179	SFLEFVIPVLVAYFNWNIYWSLWKRDHLSSRCQSHGPLTAVSSNICGHSFGRLLSSRRSL	238	
Qy	241	PLCKESAASRHSSESPRKSSILVSLRTHMNSIYAFKVGSPWRSESAALQOREVAYELRG	300	
Db	239	SASTEVPASPHSERQORRKSILMFSSRTKNSNTIASKMGFSQSDSVALLHQREHVELLR	298	
Qy	301	RKLARSAILLSAFACIWPAPCYLFTIVLSTYPRTERPKSVWYSYAFWLQWNSFVNPNPLY	360	
Db	299	RLAKLSAILLGVAFCVAPCYSLFTIVLSFYSSATGPKSVWYRYAFWLQWNSFVNPNPLY	358	
Qy	361	PLCHRRFQKAFKWLICVTYKVPALSQ-NQSVSS	391	
Db	359	PLCHRRFQKAFKIFCIKKQPLPQSHRSVSS	390	

Search completed: May 24, 2006, 13:40:59
Job time : 198 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:32:11 ; Search time 25 Seconds
(without alignments)
1504.830 Million cell updates/sec

Title: US-10-626-445-8
Perfect score: 2048
Sequence: 1 MSSNSTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1370.5	66.9	390	2 JC7566	histamine H4 recep
2	413	20.2	460	2 S09508	muscarinic acetyl
3	413	20.2	460	2 A24325	muscarinic acetyl
4	410.5	20.0	531	2 JT0531	muscarinic acetyl
5	410.5	20.0	590	2 S01114	muscarinic acetyl
6	410	20.0	460	2 I51837	muscarinic recept
7	410	20.0	460	2 A29514	muscarinic acetyl
8	409.5	20.0	590	2 S47572	muscarinic acetyl
9	403	19.7	589	2 A29476	muscarinic acetyl
10	402.5	19.7	590	2 S10128	muscarinic acetyl
11	402	19.6	589	2 B29514	muscarinic acetyl
12	401	19.6	639	2 A55019	muscarinic acetyl
13	400	19.5	460	2 A31897	muscarinic acetyl
14	399.5	19.5	532	2 JT0530	muscarinic acetyl
15	392.5	19.2	477	2 S71323	alpha-1A adrenergi
16	392	19.1	490	2 A35546	muscarinic acetyl
17	390.5	19.1	400	2 G00013	D3 dopamine recept
18	390.5	19.1	501	2 JH0447	alpha-1A-adrenergi
19	389.5	19.0	400	2 G01977	d3 dopamine recept
20	389.5	19.0	515	2 A40491	alpha-1-adrenergi
21	388.5	19.0	491	2 A41632	histamine H1 recep
22	388.5	19.0	572	2 I39369	alpha-1A-adrenergi
23	386.5	18.9	487	2 JC2495	histamine H1 recep
24	385.5	18.8	488	2 I56507	histamine H1 recep
25	384.5	18.8	517	2 A45121	alpha-1B adrenergi
26	382.5	18.7	560	2 A38731	alpha-1A adrenergi
27	382	18.7	479	2 S10127	muscarinic acetyl
28	380.5	18.6	466	2 S10126	muscarinic acetyl
29	380.5	18.6	501	2 T18863	hypothetical prote

30	380	18.6	432	2 I50829	alpha 2-adrenoccept
31	380	18.6	466	2 A40972	muscarinic acetyl
32	379.5	18.5	466	2 JH0197	muscarinic acetyl
33	379.5	18.5	466	2 S10856	muscarinic acetyl
34	379.5	18.5	515	2 JC1525	alpha-1B-adrenergi
35	379	18.5	486	2 JC1415	histamine H1 recep
36	379	18.5	479	2 JC6178	serotonin receptor
37	376	18.4	478	2 C29514	muscarinic acetyl
38	374.5	18.3	479	2 S33776	muscarinic acetyl
39	369.5	18.0	466	2 A27386	muscarinic acetyl
40	367.5	17.9	366	2 A47321	serotonin receptor
41	367	17.9	484	2 S48657	muscarinic acetyl
42	366.5	17.9	484	2 S58868	G protein-coupled
43	366	17.9	466	2 A35375	alpha-1-adrenergi
44	364.5	17.8	366	2 A47385	serotonin receptor
45	360.5	17.6	366	2 S26048	serotonin receptor

ALIGNMENTS

RESULT 1

JC7566
histamine H4 receptor, HH4R - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: JC7566
R;Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.
Biochem. Biophys. Res. Commun. 279, 615-620, 2000
A/Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.
A/Reference number: JC7566, MUID: 20568725; PMID:11118334
A/Contents: Leukocyte
A/Accession: JC7566
A/Molecule type: mRNA
A/Residues: 1-390 <NAK>
A/Cross-references: UNIPROT:Q9H3N8; UNIPARC:UPI0000039A92; DDBJ:AB045370
C/Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled
C/Genetics:
A/Gene: hh4r
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match		66.9%	Score 1370.5;	DB 2;	Length 390;
Best Local Similarity		68.1%	Pred. No. 1.4e-111;		
Matches		267;	Conservative	40;	Mismatches 82; Indels 3; Gaps 2;
Qy	1	MSSNSTGILPPAAQVPLAFIMVGNAAVILAFVVDRLRHSRYFFLNLAIS	60		
Db	1	MPDNTNINLSLSTPRVTLAFFMISLVAFAIMGNALVILAFVVDKRLRHSRYFFLNLAIS	60		
Qy	61	DFLVGLISILYIPIHVLFPNNFGSGICMFWLITDYLICTASVYNIIVLISYDRYQSVSNV	120		
Db	61	DFVGVVISILYIPIHVLFEWDFGKEICVFWLITDYLICTASVYNIIVLISYDRYLSVSNV	120		
Qy	121	SYRAQHTGIWKIVQAQVAVVILAFVNGPMTLASDSWKNSTNTKDCPGFTVEWILIT	180		
Db	121	SYRQHTGVLUKIVTLVAVVAVVILAFVNGPMTLASDSWKNSTNTKDCPGFTVEWILIT	178		
Qy	181	MLLEFLPVSIVAFNVQIVYSLWKRRALSRCPHAGFTTSSASGHLHRAGVACRTSN	240		
Db	179	SFLFVPIVILVAFVNNIYWSLWKRDHLSRQCQSHGLTAVSSNICGHSFGRLLSSRRSL	238		
Qy	241	PLGKESAAHSRHSRRKSSILVSLRTHMSSITAFKVGSPWRSESALRQREVAELLRG	300		
Db	239	SASTEVPAFHSRQRKSSLMFSSRTKMSNTIASXMGSPSQSDSVALHQREVELLRA	298		
Qy	301	RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY	360		
Db	299	RLAKLSAILLGVAVCWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPLY	358		
Qy	361	PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS	391		
Db	359	PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS	390		

RESULT 2

S09508
muscarinic acetylcholine receptor M1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S09508; S06327; S04326
R;Chapman, C.G.; Browne, M.J.
Nucleic Acids Res. 18, 2191, 1990
A;Title: Isolation of the human m1 (Hml) muscarinic acetylcholine receptor gene by PCR
A;Reference number: S09508
A;Accession: S09508
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-460 <CHA>
A;Cross-references: UNIPROT:P11229; UNIPARC:UPI00001252AB; EMBL:X52068; NID:g34450; PIDN: A24325
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
R;Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.
Nucleic Acids Res. 15, 10604, 1987
A;Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.
A;Reference number: S06327; MUID:88096607; EMBL:3697105
A;Accession: S06327
A;Molecule type: DNA
A;Residues: 1-460 <ALL>
A;Cross-references: UNIPARC:UPI00001252AB; GB:X00508; NID:g297405; PIDN:CAA68
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of two human muscarinic acetylcholine receptor subtypes.
A;Reference number: S04326; MUID:88166632; EMBL:3443095
A;Accession: S04326
A;Molecule type: DNA
A;Residues: 1-172, 'M', 174-460 <PER>
A;Cross-references: UNIPARC:UPI000005040F; EMBL:X15263; NID:g32317; PIDN:CAA33334.1; PIDN: A24325
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatase
F;25-50/Domain: transmembrane #status predicted <TM1>
F;62-93/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;142-168/Domain: transmembrane #status predicted <TM4>
F;187-209/Domain: transmembrane #status predicted <TM5>
F;367-387/Domain: transmembrane #status predicted <TM6>
F;402-420/Domain: transmembrane #status predicted <TM7>
F;2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.28; Score 413; DB 2; Length 460;
Best Local Similarity 27.4%; Pred. No. 3.7e-28;
Matches 122; Conservative 84; Mismatches 150; Indels 90; Gaps 19;
QY 5 NSTGILPPAAQVPLAFL---MSSFAFAMVGNVAVILAFVVDNRLHRSNYFFFLNLAISD 61
DB 12 NITVLAPGKGPQVAFIGITITGLLSLATVGNLLVLSFKVNTLKTNNYFLLSLACAD 71
QY 62 FLVGLISIPLYIPHLV-FNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120
DB 72 LIIGTFSMNLYTYLLMGHWALGTACDLWLALDYVNASVNMNLLISFDYFSVTRPL 131
QY 121 SYRAQHTGIMKIVAQMVAW-VILAFVNGPMILASDSWKNSNTK-----DCEPGFVTEW 174
DB 132 SYRAKRT--PRRAALMIGLAWLSFVLWAPAIL---FWQVLVGRTVLAGQCIQFLSQP 186
QY 175 YILITITMLLEFLLPVISVAYFNQIYWSLWKR-----RAL-----SRCPSHAGSTSSS 224
DB 187 IIFGTAMAAFLPVTVMC---TLYWRIYRETNRRARELAALQGSPTPGKGGSSSSSE 242
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAASHSESPPRK 258
DB 243 RSQPGAGSGPETPPGRCCR---CCRAPRLLOQVSWKEEEDSGMESLTSSEGEEP--G 297
QY 259 SSILVSL-----RTHMNSSITAFKVGFWRSESA-----ALRQREY 294
DB 298 SEVVIKPMVDPEAQAPKQPPRSSPNTVKRPTKGRAGKQKPRGKQAKRKT 354
QY 295 AELLRGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVVSYAFMLQWENSF 354

DB 355 FSLVKEKKAARTLSAILLAPILTWTPYNIWLV-STFKDCVPETLW-ELGYWLCYVNST 412
QY 355 VNPFLYPLCHRRRFQKAFWKILCVTKW 380
DB 413 INPMCALCNKAFRDTF-RLLLLCRW 437

RESULT 3

A24325
muscarinic acetylcholine receptor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24325
R;Kubo, T.; Fukuda, K.; Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, T.; H
Nature 323, 411-416, 1986
A;Title: Cloning, sequencing and expression of complementary DNA encoding the muscarinic
A;Reference number: A24325; MUID:87014801; EMBL:3762692
A;Accession: A24325
A;Molecule type: mRNA
A;Residues: 1-460 <KUB>
A;Cross-references: UNIPROT:P04761; UNIPARC:UPI00001252AD; GB:X04413; NID:g1863; PIDN: A24325
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatase
F;25-50/Domain: transmembrane #status predicted <TM1>
F;62-93/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;142-168/Domain: transmembrane #status predicted <TM4>
F;187-209/Domain: transmembrane #status predicted <TM5>
F;367-387/Domain: transmembrane #status predicted <TM6>
F;402-420/Domain: transmembrane #status predicted <TM7>

Query Match 20.2%; Score 413; DB 2; Length 460;
Best Local Similarity 27.5%; Pred. No. 3.7e-28;
Matches 122; Conservative 83; Mismatches 154; Indels 84; Gaps 18;
QY 5 NSTGILPPAAQVPLAFL---MSSFAFAMVGNVAVILAFVVDNRLHRSNYFFFLNLAISD 61
DB 12 NITVLAPGKGPQVAFIGITITGLLSLATVGNLLVLSFKVNTLKTNNYFLLSLACAD 71
QY 62 FLVGLISIPLYIPHLV-FNNFGSGICMFWLITDYLCTASVNVILISYDRYQSVSNV 120
DB 72 LIIGTFSMNLYTYLLMGHWALGTACDLWLALDYVNASVNMNLLISFDYFSVTRPL 131
QY 121 SYRAQHTGIMKIVAQMVAW-VILAFVNGPMILASDSWKNSNTK-----DCEPGFVTEW 174
DB 132 SYRAKRT--PRRAALMIGLAWLSFVLWAPAIL---FWQVLVGRTVLAGQCIQFLSQP 186
QY 175 YILITITMLLEFLLPVISVAYFNQIYWSLWKR-----RAL-----SRCPSHAGSTSSS 224
DB 187 IIFGTAMAAFLPVTVMC---TLYWRIYRETNRRARELAALQGSPTPGKGGSSSSSE 242
QY 225 AS-----GHLHRAGVACRT-----SNPGLKESAASHSESPPRK 258
DB 243 RSQPGAGSGPETPPGRCCR---CCRAPRLLOQVSWKEEEDSGMESLTSSEGEEP--G 297
QY 259 SSILVSL-----RTHMNSSITAFKVGFWRSESA-----ALRQREY 297
DB 298 SEVVIKPMVDPEAQAPKQPPRSSPNTVKRPTKGRAGKQKPRGKQAKRKT 357
QY 298 LRGKRLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVVSYAFMLQWENSF 357
DB 358 VKEKKAARTLSAILLAPILTWTPYNIWLV-STFKDCVPETLW-ELGYWLCYVNSTINP 415
QY 358 FLPLCHRRRFQKAFWKILCVTKW 380
DB 416 MCYALCNKAFRDTF-RLLLLCRW 437

RESULT 4

JT0531
muscarinic acetylcholine receptor M5 - rat
C;Species: Rattus norvegicus (Norway rat)

Qy	306	SLAIISSAFACWAPYCLFTTIVLSYPTPRPKSVVYSIAFWLQFNSFNPLYPILCHR	365
Dd	442	TLSAILALAFITWTPIYNIMLV-STFDCKCPVTLMH-LGYWLVCYNSTNPICAYLCNR	499
Qy	366	RFOKAFWKILCVTKM	380
Dd	500	TFRKTF-KLLLLCRW	513
 RESULT 5 S01114			
muscarinic acetylcholine receptor M2, glandular - pig			
N;Alternate names: muscarinic acetylcholine receptor III			
C;Species: Sus scrofa domestica (domestic pig)			
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004			
C;Accession: S01114			
R;Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.			
FEBS Lett. 235, 257-261, 1988			
A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonist			
A;Reference number: S01114; MUID:88296835; PMID:3402600			
A;Accession: S01114			
A;Molecule type: DNA			
A;Residues: 1-590 <AKI>			
A;Cross-references: UNIPROT:P11483; UNIPARC:UPI0000125287; EMBL:X12712; NID:g1861; PIDN:C			
C;Superfamily: vertebrate rhodopsin			
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem			
F	68-91/Domain:	transmembrane #status predicted <TM1>	
F	105-125/Domain:	transmembrane #status predicted <TM2>	
F	143-164/Domain:	transmembrane #status predicted <TM3>	
F	185-207/Domain:	transmembrane #status predicted <TM4>	
F	231-252/Domain:	transmembrane #status predicted <TM5>	
F	493-513/Domain:	transmembrane #status predicted <TM6>	
F	528-546/Domain:	transmembrane #status predicted <TM7>	
 Query Match 20.0%; Score 410.5; DB 2; Length 590; Best Local Similarity 24.8%; Pred. No. 8e-28; Matches 125; Conservative 82; Mismatches 136; Indels 161; Gaps 16;			
Qy	18	LAFILMSFAFAIMGVNAVILAFVVDRNLRLRSNYFFLNLAISDFVLGLISIPLYIPHVL	77
Dd	71	I AFTIGIALVTIIGNILVIAFKVKQLKTNNYFLSLACADLIIGVISNMFLTYYII	130
Qy	78	FN-WNFSGGICMFMLITDYLCTASVYNVILSYDRYOSVSNAVSRAOHT----	GIMKI 132
Dd	131	MNRWALGNLACDLMLSIDYASNASVMNLLVISFDIFYESITRPLTYRAKRTTKRAGWMIG	190
Qy	133	VQMVAWVILAFLVNGPMLASDSWNKSNNTYKCEPG-----FVTEWYILTITMLEFLL	187
Dd	191	LA-----WVISFILWAPAIL----FMQYFVGKRTVPVGGECFIQFLSEPTITFGTAIAAFYM	242
Qy	188	PVISVAVENVQIYWSLKRRALSRCPSHAGF--STTSSSASGHLAGRVACRTSNPGLKE	245
Dd	243	PVTIMTI-----LYRWIKYTEB-KRTKELAGLOASTEAENFVHPGTGSRCSSYELOQ	297
Qy	246	SASR-----HSES-----	254
Dd	298	QSLKESARRKYGRCHFETTKSWKPESAQMDDHSSSDSNWNDAASAENSASSDEEDI	357
Qy	255	---PRRKSSILVSRTHNW-----SSITAFKV----	278
Dd	358	GSETRAIYSIVKLPGHSTILNSTKLPSNDNLQPVEELGTVDLERKASKLOAKSMDDG	417
Qy	279	GSFWR-----ESAA-----LRQ	291
Dd	418	GSFOKSFSLPIQIESAVDTAKADVNSVGKTTATLPISFKEATLAKRFALKTRSQITK	477
Qy	292	REVAELIRGRKLARSAILLSAFAICWAPYCLFTTIVLSYPTPRPKSVVYSIAFWLQWF	351
Dd	478	KRMSLIKEKAQTLSAILALAFITWTPIYNIMLV-NTFCDSCIPKTYM-NLGWLYCYI	535
Qy	352	NSFVNPLYPLCHRRFQKAFWKIL	375
Dd	536	NSTNPPVCYALCNKTRFTTFKML	559

A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Reference number: A94293; MUID:87263421; PMID:3037705
A;Accession: A94293
A;Molecule type: mRNA
A;Residues: 1-227;338-460 <B02>
A;Cross-references: UNIPARC:UPI00001778CE; UNIPARC:UPI00001778CF
A;Experimental source: cerebral cortex
A;Note: only a part of the protein translation is given; none of the nucleotide sequence is given
R;Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues in
A;Reference number: A37121; MUID:90337982; PMID:2380182
A;Accession: A37121
A;Status: preliminary
A;Molecule type: protein
A;Residues: 62-124 <KUR>
A;Cross-references: UNIPARC:UPI00001778D0
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C
F;25-50/Domain: transmembrane #status predicted <TM1>
F;62-93/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;142-168/Domain: transmembrane #status predicted <TM4>
F;187-209/Domain: transmembrane #status predicted <TM5>
F;367-387/Domain: transmembrane #status predicted <TM6>
F;402-420/Domain: transmembrane #status predicted <TM7>
F;2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.0%; Score 410; DB 2; Length 460;
Best Local Similarity 27.4%; Pred. No. 6.7e-28;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;

QY 5 NSTGILPPAAQVPLAFL--MSSFAFAMVGNVAVILAFVVDNRLHRSNVFFLNLAISD 61
DB 12 NITVLAQKGPQVAFIGITGLLSLATVGNLLVLSFKVNTLKVNNYFLLSLACAD 71
QY 62 FLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVNAV 120
DB 72 LIIGTFSMNLYTYLLGHGHALGTACDLMLALDYVNASVMNLLISDFRYSVTRPL 131
QY 121 SYRAQHTGINKIVAQWAV-WILAFVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
DB 132 SYRAKRT--PRRAALMIGLAWLVSFVLWAPAIL---FWQYLVGERTVLAQCQYIQLSQP 186
QY 175 YLITITMLLEFLPLVISVAVFNVIYSLWKR-----RAL-----SRCPSHAGPSTSSS 224
DB 187 IITFGTMAAFYLPVTVMC-----TLWRIYRETNARALAAQSGSTPGKGGSSSSE 242
QY 225 AS-----GHLHRAGVACRT-----RTHMSSITAFKVSFWSES-----ALRQREY 294
DB 243 RSQPGAEGSPESPPGCCR---CCRAPLLQAYSWKEEEDSGMESLTSSEGEEP--G 297
QY 259 SSILVSL-----RTHMSSITAFKVSFWSES-----ALRQREY 294
DB 298 SEVVIKMPVDSQAQPTKPPKSSPNTVRPTKKG---RDRGKGQKPKGKQAKRKT 354
QY 295 AEILGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSF 354
DB 355 FSLVKEKAARTLSAILLAFILTWTPNIMVLV-STFCKDCVPETLM-ELGYWLCYNST 412
QY 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
DB 413 VNPWCYALCNKAPRDTF-RLLLLCRW 437

RESULT 8
S47572
muscarinic acetylcholine receptor m3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47572
R;Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
Biochim. Biophys. Acta 1223, 151-154, 1994

RESULT 6
151837
muscarinic receptor - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: 151837
R;Lai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske
Adv. Exp. Med. Biol. 287, 313-330, 1991
A;Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy
A;Reference number: 151837; MUID:92101806; PMID:1759615
A;Accession: 151837
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-460 <RES>
A;Cross-references: UNIPARC:UPI0000046CE7; GB:S73971; NID:9241253; PIDN:AAB20705.1; PID:
C;Genetics:
A;Gene: m1
C;Superfamily: vertebrate rhodopsin

Query Match 20.0%; Score 410; DB 2; Length 460;
Best Local Similarity 27.4%; Pred. No. 6.7e-28;
Matches 122; Conservative 83; Mismatches 151; Indels 90; Gaps 19;

QY 5 NSTGILPPAAQVPLAFL--MSSFAFAMVGNVAVILAFVVDNRLHRSNVFFLNLAISD 61
DB 12 NITVLAQKGPQVAFIGITGLLSLATVGNLLVLSFKVNTLKVNNYFLLSLACAD 71
QY 62 FLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVNAV 120
DB 72 LIIGTFSMNLYTYLLGHGHALGTACDLMLALDYVNASVMNLLISDFRYSVTRPL 131
QY 121 SYRAQHTGINKIVAQWAV-WILAFVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
DB 132 SYRAKRT--PRRAALMIGLAWLVSFVLWAPAIL---FWQYLVGERTVLAQCQYIQLSQP 186
QY 175 YLITITMLLEFLPLVISVAVFNVIYSLWKR-----RAL-----SRCPSHAGPSTSSS 224
DB 187 IITFGTMAAFYLPVTVMC-----TLWRIYRETNARALAAQSGSTPGKGGSSSSE 242
QY 225 AS-----GHLHRAGVACRT-----RTHMSSITAFKVSFWSES-----ALRQREY 294
DB 243 RSQPGAEGSPESPPGCCR---CCRAPLLQAYSWKEEEDSGMESLTSSEGEEP--G 297
QY 259 SSILVSL-----RTHMSSITAFKVSFWSES-----ALRQREY 294
DB 298 SEVVIKMPVDSQAQPTKPPKSSPNTVRPTKKG---RDRGKGQKPKGKQAKRKT 354
QY 295 AEILGRKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSF 354
DB 355 FSLVKEKAARTLSAILLAFILTWTPNIMVLV-STFCKDCVPETLM-ELGYWLCYNST 412
QY 355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
DB 413 VNPWCYALCNKAPRDTF-RLLLLCRW 437

RESULT 7
A29514
muscarinic acetylcholine receptor M1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A94518; A94293; A37121; A29514
R;Bonner, T.I.
submitted to GenBank, July 1987
A;Reference number: A94518
A;Accession: A94518
A;Molecule type: mRNA
A;Residues: 1-460 <B01>
A;Cross-references: UNIPROT:P08482; UNIPARC:UPI0000046CE7
R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987


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Qy 18 LAFLMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPYIPIHVL 77
Db 71 IAFITGILALVTIIGNILVIVSPKVNKQLTNNYVFLSLACADLIIGVISMNLFTTYII 130
Qy 78 FN-WNFGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVNAVSYRAQHT-----GIMKI 132
Db 131 MNRWALGNLACDLWLADLDYVNASVNVNLLVISDFRYFSITRPLTYRAKRTTKRAGVMIG 190
Qy 133 VAQNVAVILAFVNGPMILASDSWKNSTNTKDCPEG-----FVTEWVILTIWMLLEFLL 187
Db 191 LA-----WVISFVLWAPAIL---FWQYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYM 242
Qy 188 PVISVAVNFQIYWSLWK-----FVTEWVILTIWMLLEFLL 205
Db 243 PVIIMTI-----LYWRIYKETEKTRELQAGSQTEAETENFVHPTGSSRSCSSYELQQQ 298
Qy 206 -----RRALSRCPESHAGFTT-----SSASGHLHRAGVACRTSNPGLKES 246
Db 299 SMKRSNRKYGRC--HFWFTTKSWKPSSEQMDQDHSSDSWNNNDAAAASLENSASSDEED 356
Qy 247 AASR-----HS----- 252
Db 357 IGSETRAIYIVLKLPGHSTILNSTKLPSNDLQVPHEELGMVDLERKADKLOAQKSVD 416
Qy 253 --ESPRLKSGILVSLR-----THMNSSI-----TAFKVGSSAALR 290
Db 417 GGSFPKFSKLPIQLESADVDTAKTSDVNSSVGKSTALPLSFKEATLAKRFALKTRSQIT 476
Qy 291 OREYAEALLRGRKLARSAILLSAIPAICWAPYCLPTIVLSTYPRTERPKSVWYSIAFWLOW 350
Db 477 KRKRMSLVKEKKAQTLAISAILLAFIITWTPYINMLV-NTFCDSCIPKTFW-NLGYWLVCY 534
Qy 351 FNSFVNPFLYPLCHRRFQKAFWKIL 375
Db 535 INSTVNPVVCALCNKTRTFTFKMLL 559

RESULT 11
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muscarinic acetylcholine receptor M3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: B94518; B94293; B37121; B29514
R;Bonner, T.I.
submitted to GenBank, July 1987
A;Reference number: A94518
A;Accession: B94518
A;Molecule type: mRNA
A;Residues: 1-589 <B01>
A;Cross-references: UNIPROT:P08483; UNIPARC:UPI0000163B75
R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Reference number: A94293; MUID:87263421; PMID:3037705
A;Accession: B94293
A;Molecule type: mRNA
A;Residues: 1-269;463-589 <B02>
A;Cross-references: UNIPARC:UPI00001778C1; UNIPARC:UPI00001778C2
A;Experimental source: cerebral cortex
A;Note: only a part of the protein translation is given; none of the nucleotide sequence
R;Kurténbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invc
A;Reference number: A37121; MUID:90337982; PMID:2380182
A;Accession: B37121
A;Status: preliminary
A;Molecule type: protein
A;Residues: 104-166 <KUR>
A;Cross-references: UNIPARC:UPI00001778C3
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F;67-90/Domain: transmembrane #status predicted <TM1>
F;104-124/Domain: transmembrane #status predicted <TM2>
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F;184-206/Domain: transmembrane #status predicted <TM4>
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F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6;15;41;48;52/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local Similarity 23.8%; Pred. No. 4.4e-27;
Matches 125; Conservative 84; Mismatches 145; Indels 172; Gaps 15;
Qy 4 SNTGILPPAAQ-----VPLAFMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFLNLA 58
Db 51 SNTDSSDPLGGHTIMQVVFIAFLTGLFALVTIIGNILVIVAFKVNKQLTNNYVFLSLA 110
Qy 59 ISDFLVGLISIPYIPIHVLFN-WNFGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVS 117
Db 111 CADLIIGVISMNLFTTYIIMNRWALGNLACDLWLSIDYVNASVNMLLVISDFRYFSIT 170
Qy 118 NAVSYRAQHT-----GIMKI VAVNVAVILAFVNGPMILASDSWKNSTNTKDCPEG--- 169
Db 171 RPLTYRAKRTTKRGVMIGLA-----WVISFVLWAPAIL---FWQYFVGKRTVPPGECFI 222
Qy 170 -FVTEWVILTIWMLLEFLLPVI SVAYFNVOIYWSLWKRRALSRCPESHAGF--STTSSAS 226
Db 223 QFLSEPTITFGTAIAAFYMPVIMTI-----LYWRIYKETE-KRTKELAGLQAGSQTEAEAE 277
Qy 227 GHLHRAGVACRTSNPGIKESAAHRHSESPPRK-----SSILVSLRTHMNSSI----- 258
Db 278 NFVHPTGSSRSCSSYELQQGVKR-----SSRKYGRCHFVFTTKSWKPSAQMDQDHSDD 334
Qy 259 -----SWNNDDAAAASLENSASSDEEDIGSETRAIYIVLKLPGHSSILNSTKLPSNDLQVSNED 394
Db 274 -----TAFKVGSSFWSESAA----- 288
Qy 395 LGTVDVVERNAHKLQAKSMGDGNCQKDFTKLPIQLLESADVDTGKTSNTSSADKTTATLP 454
Db 289 -----LRQREYAEALLRGRKLARSAILLSAIPAICWAPYCLPTIVLS 329
Qy 455 LSPKEATLAKRFALKTRSQITKRRKMSLIEKKAQTLAISAILLAFITWTPYINMLV-N 513
Qy 330 TYPRTERPKSVWYSIAFWLQWFNFSFVNPFLYPLCHRRFQKAFWKIL 375
Db 514 TPCDSCIPKTYW-NLGYWLVCYINSTVNPVVCALCNKTRTFTFKELL 558

RESULT 12
A55019
muscarinic acetylcholine receptor, M3 isoform - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A55019
R;Gadbut, A.P.; Galper, J.B.
J. Biol. Chem. 269, 25823-25829, 1994
A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium ar
A;Reference number: A55019; MUID:95014393; PMID:7929287
A;Accession: A55019
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-639 <GAD>
A;Cross-references: UNIPROT:P49578; UNIPARC:UPI00001252B4; GB:L10617; NID:9530097; PID
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
Query Match 19.6%; Score 401; DB 2; Length 639;
Best Local Similarity 24.4%; Pred. No. 5.9e-27;
Matches 124; Conservative 84; Mismatches 136; Indels 164; Gaps 16;
Qy 16 VPLAFMSSFAFAMVGNVAVILAFVVDNRNLHRSNYFFLNLAISDFLVGLISIPYIPIH 75
Db 117 VLIAFLTGIIALVTIIGNILVIVSVKVNKQLTNNYVFLSLACADLIIGVISMNLFTTY 176
```


Job time : 26 secs

```
QY 214 ----SHAGFTT---SSASGHLHRAG-----VACRT-----SNPGLK 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 263 QRENNQASWSSRRSSTTGKPSQATGPSANWAKAEQLTTCSSVPSSEDEKPADPVLQ 322
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 ESAASHSESPPRKSSILVSLRTHMSSI---TAPKVGSWRSESALR-----290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 323 VVYKSQKESPGSEFSAEETEETFVKAETKSDYDTPNYLLSPAAHRPKSKQCVAYKFR 382
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 -----OREYAEALLRGRKLAR 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 383 LVVKADGNQETNGCHVKIMPCFPFVAKPEPTKGLNPNPSSHQMTYKKRVVIVKERRKAAQ 442
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 306 SLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFYPLCHR 365
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 443 TLSAILLAFLITWTPYNIMLV-STPCDKCVPVTLWH-LGYWLCYVNSTVNPICYALCNR 500
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 366 RFQKAFWKILCVTKW 380
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 501 TFRKTF-KMLLLCRW 514
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 15

S71323
alpha-1A adrenergic receptor - Japanese medaka
C;Species: Oryzias latipes (Japanese medaka)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C;Accession: S71323
R;Tasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996
A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me
A;Reference number: S71323; MUID:96184522; PMID:8654394
A;Accession: S71323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <YAS>
A;Cross-references: UNIPARC:UPI0000177BAD; EMBL:D63859
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
C;Superfamily: vertebrate rhodopsin

```
Query Match          19.2%; Score 392.5; DB 2; Length 477;
Best Local Similarity 28.0%; Pred. No. 2.3e-26;
Matches 115; Conservative 65; Mismatches 145; Indels 85; Gaps 15;

QY 4  SNGTGILPP-----AAQVPLAFLMSFAPAFMVGNAVIVLAFVVDNRNLRHSNYFFNLAI 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 SNGSHVLAPELNTVKAIVLGVLGIFILFGVIGNILVLSVVCHEHLQTVTYFIVNLAV 77
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 SDFLVGLISIP-L-YIPHVLNFWNPGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVN 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 ADLLSSTVLFPFSAIFELDRWVGRVFCNIWAADVLCCTASTMSLCVISVDRIYIGVSY 137
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 AVSYRAQHTGIMKIVAOQWAVVILLAFVN-GPMILASDSWKNSTNTKD--C---EPGFV 171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 PLRYPAIMTKRRALLAVML-LWVLSVLIISITGPLF----GWKEPADEDETCKITEEPGYA 192
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 TEWILITITMLLEFLLPVISVAYFNVQIYNSLMKRRALSRCPSHAGFSTTSSASGHLHR 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 -----IFSAGVSFYLPAIILAMYCRVY-----215
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 AGVACRTSNFGLKESASRHSPPRKSSILVSLRTHMSSIITAFKVGSWRSESALRQ 291
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 --VVAQKESRGLKEGQIKESDSQ-----VILMRHGNTTV-----SEDEALRS 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 REYAE-----LRGRKLARSAILLSAFACWAPYCLFTIVLSTYPRTERPKSVWYSIAF 346
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 RTHFALRLKXFSREKKAAGTIGIVVGCFLCWLFPFLVPIGSIFFP-AYRPSDTVFKITF 317
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 WLOWFNSFVNPFLPLCHRRFQKAFWKIL---CVTKWPA-----LSQNQS 388
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 318 WLGFNSCINPIIYLCNQEFKKAQFQSLGLGVHCLRWTPRAHHHLSVGQS 367
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: May 24, 2006, 13:35:04

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2006, 13:31:50 ; Search time 147 Seconds
(without alignments)
2460.416 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSESNSGTILPPAAQVPLAF.....WKILCVTKWPAALSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result #	No.	Score	Query Match	Length	DB	ID	Description
1	1	2035	99.4	391	2	Q91ZY2_MOUSE	Q91ZY2 mus musculus
2	2	1745	85.2	391	2	Q91ZY1_RAT	Q91ZY1 rattus norv
3	3	1372.5	67.0	390	2	Q96LD9_HUMAN	Q96LD9 homo sapien
4	4	1372	67.0	262	2	Q2M2N7_MOUSE	Q2M2N7 mus musculus
5	5	1370.5	66.9	390	1	HRH4_HUMAN	Q9H3P8 homo sapien
6	6	1370.5	66.9	390	2	Q4G0I6_HUMAN	Q4G0I6 homo sapien
7	7	1357.5	66.3	390	2	Q3V8G8_MACFA	Q3V8G8 macaca fasc
8	8	1311.5	64.0	390	2	Q8WNV9_PIG	Q8WNV9 sus scrofa
9	9	1238	60.4	389	2	Q91ZY3_CAVPO	Q91ZY3 cavia porce
10	10	733.5	35.8	414	2	QARKY3_TETNG	QARKY3 tetraodon n
11	11	722.5	35.3	445	1	HRH3_HUMAN	Q9Y5N1 homo sapien
12	12	722.5	35.3	445	2	Q448M6_HUMAN	Q448M6 homo sapien
13	13	721	35.2	445	1	HRH3_CAVPO	Q9J135 cavia porce
14	14	718.5	35.1	445	2	Q865B1_MACMU	Q865B1 macaca mula
15	15	716.5	35.0	445	1	HRH3_RAT	Q9GYN8 rattus norv
16	16	715.5	34.9	445	1	HRH3_MOUSE	P8A406 mus musculus
17	17	715.5	34.9	445	2	Q540F3_MOUSE	Q540F3 mus musculus
18	18	713.5	34.8	445	2	Q5G535_PHOSU	Q5G535 phodopus su
19	19	712.5	34.8	341	2	Q4RVG9_TETNG	Q4RVG9 tetraodon n
20	20	709.5	34.6	413	2	Q541U0_RAT	Q541U0 rattus norv
21	21	704.5	34.4	473	2	Q2MZ33_BRARE	Q2MZ33 brachydanio
22	22	700.5	34.2	406	2	Q3USH0_MOUSE	Q3USH0 mus musculus
23	23	691.5	33.8	406	2	Q5G534_PHOSU	Q5G534 phodopus su
24	24	665.5	32.5	365	2	Q8WY01_HUMAN	Q8WY01 homo sapien
25	25	665.5	32.5	373	2	Q8WXZ9_HUMAN	Q8WXZ9 homo sapien
26	26	591	28.9	497	2	Q2VJ18_RAT	Q2VJ18 rattus norv
27	27	584	28.5	465	2	Q2VJ17_RAT	Q2VJ17 rattus norv
28	28	569	27.8	344	2	Q5PPG3_RAT	Q5PPG3 rattus norv
29	29	547	26.7	174	2	Q6J9J4_9PRIM	Q6J9J4 gorilla gor
30	30	543	26.5	175	2	Q6J9J5_PANTR	Q6J9J5 pan troglod
31	31	492.5	24.0	301	2	Q8WY00_HUMAN	Q8WY00 homo sapien

32	492.5	24.0	309	2	Q8NI49_HUMAN	Q8NI49 homo sapien
33	443	21.6	443	2	Q4SAC4_TETNG	Q4SAC4 tetraodon n
34	418	20.4	460	1	ACM1_MACMU	P56489 macaca mula
35	417.5	20.4	584	2	Q61W39_CAEBR	Q61W39 caenorhabdi
36	416	20.3	481	2	Q5U3D9_BRARE	Q5U3D9 brachydanio
37	415.5	20.3	530	2	Q8VH24_CAVPO	Q8VH24 cavia porce
38	414.5	20.2	532	1	ACM5_MACMU	P56490 macaca mula
39	413	20.2	454	2	Q96RH1_HUMAN	Q96RH1 homo sapien
40	413	20.2	460	1	ACM1_HUMAN	P11229 homo sapien
41	413	20.2	460	1	ACM1_PIG	P04761 sus scrofa
42	413	20.2	460	2	Q53XZ3_HUMAN	Q53XZ3 homo sapien
43	413	20.2	460	2	Q5R949_PONPY	Q5R949 pongo pygma
44	410.5	20.0	502	2	Q4PLW4_LEPMA	Q4PLW4 lepomis mac
45	410.5	20.0	531	1	ACM5_RAT	P08911 rattus norv

ALIGNMENTS

RESULT 1
Q91ZY2_MOUSE
ID Q91ZY2_MOUSE PRELIMINARY; PRT; 391 AA.
AC Q91ZY2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 23.
DE Histamine H4 receptor.
GN Name=Hrh4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AF358859; AAK97380.1; -; mRNA.
CC Ensembl; ENSMUSG00000037346; Mus musculus.
CC MGI; MGI:2429635; Hrh4.
CC GO; GO:0005615; C:extracellular space; RCA.
CC GO; GO:0005887; C:integral to plasma membrane; IC.
CC GO; GO:0005624; C:membrane fraction; IDA.
CC GO; GO:0004969; F:histamine receptor activity; IDA.
CC GO; GO:0001594; F:rhodopsin-like receptor activity; RCA.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; RCA.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC PANTHER; PTHR19266:SF82; Histaminrecept_H4; 1.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01726; HISTAMINEH4.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Membrane; Receptor; Transducer;
Transmembrane.
SQ SEQUENCE 391 AA; 44249 MW; 59EC73CB5214C5E0 CRC64;

Query Match 99.4%; Score 2035; DB 2; Length 391;

Best Local Similarity 99.7%; Pred. No. 2e-138;

Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSESNSGTILPPAAQVPLAF.....WKILCVTKWPAALSONQSVSS 60

Db 1 MSESNSGTILPPAAQVPLAF.....WKILCVTKWPAALSONQSVSS 60

```

QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVNVILISYDRYQSVNAV 120
Db 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVNVILISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILTIT 180
Db 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILTIT 180
QY 181 MLLEFLLPVLISVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
Db 181 MLLEFLLPVLISVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
QY 241 PGLKESAAHSRSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWESESAALRQREVAELLRG 300
Db 241 PGLKESAAHSRSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWESESAALRQREVAELLRG 300
QY 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISAFWLNWFNSFVNPFLY 360
Db 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISAFWLNWFNSFVNPFLY 360
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 2
C912YL RAT
ID Q91ZY1_RAT PRELIMINARY; PRT; 391 AA.
AC Q91ZY1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 22.
DE Histamine H4 receptor.
GN Name:Hrh4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN NCBI_TaxID=10116;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AF358860; AAK97381.1; -; mRNA.
CC Ensembl; ENSRNOG0000016887; Rattus norvegicus.
CC RGD; 620631; Hrh4.
CC GO; GO:0004969; F:histamine receptor activity; IDA.
CC GO; GO:0006954; P:inflammatory response; IMP.
CC GO; GO:0006276; GPCR_Rhodpsn.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC PANTHER; PTHR19266:SF82; Histamine H4 rcpt.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR01726; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Membrane; Receptor; Transducer;
CC Transmembrane.
CC SEQUENCE 391 AA; 44023 MW; C707BA6E39CFED41 CRC64;

Query Match 85.2%; Score 1745; DB 2; Length 391;
Best Local Similarity 84.9%; Pred. No. 1.5e-117;
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

QY 1 MSENSTGILPPAAQVPLAFVNGVAFVILAFVVDRLNRHRSNYFFLNLAIS 60
Db 1 MSENSTGILPPAAQVPLAFVNGVAFVILAFVVDRLNRHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVNVILISYDRYQSVNAV 120
Db 61 DFLVGLISIPLYIPHLFNNFGSGICMFWLITDYLLCTASVNVILISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILTIT 180
Db 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMLASDSWKNSNTKDCPEPGFVTEWYILTIT 180
QY 181 MLLEFLLPVLISVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
Db 181 MLLEFLLPVLISVAYFNVQIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
QY 241 PGLKESAAHSRSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWESESAALRQREVAELLRG 300
Db 241 PGLKESAAHSRSHSPRRKSSILVSLRTHMNSSITAFKVGFSFWESESAALRQREVAELLRG 300
QY 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISAFWLNWFNSFVNPFLY 360
Db 301 RKLARSLAILLSAFAICWAPYCLFTTIVLSTYPRTERPKSVWYISAFWLNWFNSFVNPFLY 360
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 3
Q96LD9 HUMAN
ID Q96LD9_HUMAN PRELIMINARY; PRT; 390 AA.
AC Q96LD9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE Histamine receptor H4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21106319; PubMed=11179435;
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
RA Rauser L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;
RT "Discovery of a novel member of the histamine receptor family.";
RL Mol. Pharmacol. 59:427-433(2001).
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AY008280; AAL09297.1; -; mRNA.
CC Ensembl; ENSG00000134489; Homo sapiens.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. ; IEA.
CC GO; GO:0007165; P:signal transduction; IEA.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR008102; Histamine H4 rcpt.
CC PANTHER; PTHR19266:SF82; Histamine H4; 1.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR01726; HISTAMINEH4R.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Membrane; Receptor; Transducer;
CC Transmembrane.
CC SEQUENCE 390 AA; 44470 MW; CC82B5D30D216C66 CRC64;

```

Query Match 67.0%; Score 1372.5; DB 2; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.1e-90;
Matches 267; Conservative 41; Mismatches 81; Indels 3; Gaps 2;

QY 1 MSESNGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRNLHRHRSNYFFNLAI 60
DB 1 MDTNSTINLSLSTRVTLAFMGLVAFMIGNALVILAFVVDNKLHRSSYFFNLAI 60

QY 61 DFLVGLISIPLYIPIHVLFWNNFGSGICMFWLITDYLCTASVYVNLVLSYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPIHTLFEWDFGKEICVFWLITDYLCTASVYVNLVLSYDRYQSVNAV 120

QY 121 SYRAQHTGIMKIVQAVMVAWVILAFVNGPMLASDSWKNSTNTKDCPFGVTEWYILIT 180
DB 121 SYRTQHTGVILKIVTLVAVVWVLAFLVNGPMLVSESWKDRGS--ECBPFGFSEWYILAIT 178

QY 181 MLLEFLLPVSIVAYENVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSN 240
DB 179 SFLEFVPIVLVAYFNNIYWSLWKRDHLSCQSHPGLTAVSNNICHSFGRGLSSRRSL 238

QY 241 PGLKESAASHSESPPRRKSSILVSLRTHMNSSITAFKVGFSWRSESAAALQREYAEILRG 300
DB 239 SASTVPASHSESRRQKSSLMFSRTKMSNTIASKMGFSQSDSVALHQREHVELLA 298

QY 301 RKLARSAILLSAPALCWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPFLLY 360
DB 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPFLLY 358

QY 361 PLCHRRFQKAFKILCVTKWPALSO--NQSVSS 391
DB 359 FLCHRRFQKAFKILFCIKKQPLPSQHSRSVSS 390

RESULT 4
Q2M2N7 MOUSE PRELIMINARY; PRT; 262 AA.

ID Q2M2N7 MOUSE Q2M2N7;
AC Q2M2N7;
DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 21-FEB-2006, entry version 1.
DE Hrh4 protein.
GN Names=Hrh4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Rosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; BC111862; AAI11863.1; -, mRNA.
SQ SEQUENCE 262 AA; 29860 MW; 1A0CAF2085E09779 CRC64;

Query Match 67.0%; Score 1372; DB 2; Length 262;
Best Local Similarity 99.6%; Pred. No. 7.7e-91;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 130 MKTIVQAVVAVMILAFVNGPMLASDSWKNSTNTKDCPFGVTEWYILITMLLEFLLPV 189
DB 1 MKTIVQAVVAVMILAFVNGPMLASDSWKNSTNTKDCPFGVTEWYILITMLLEFLLPV 60

QY 190 ISVAYFNQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSNPGLKESAAS 249
DB 61 ISVAYFNQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSNPGLKESAAS 120

QY 250 RHESPPRRKSSILVSLRTHMNSSITAFKVGFSWRSESAAALQREYAEILRGRKLARSIAI 309
DB 121 RHESPPRRKSSILVSLRTHMNSSITAFKVGFSWRSESAAALQREYAEILRGRKLARSIAI 180

QY 310 LLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPFLLYPLCHRRFQK 369
DB 181 LLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPFLLYPLCHRRFQK 240

QY 370 AFWKILCVTKWPALSONQSVSS 391
DB 241 AFWKILCVTKWPALSONQSVSS 262

RESULT 5
HRH4_HUMAN STANDARD; PRT; 390 AA.

ID HRH4_HUMAN Q9H3N8; Q9GZQ0;
AC Q9H3N8; Q9GZQ0;
DT 01-JUN-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2001, sequence version 2.
DT 07-MAR-2006, entry version 43.
DE Histamine H4 receptor (HRH4) (GPRV53) (G-protein coupled receptor 105)
DE (GPCR105) (SP9144) (AXOR35).
GN Names=HRH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;
RA Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.;
RT "Molecular cloning and characterization of a novel type of histamine
receptor preferentially expressed in leukocytes";
J. Biol. Chem. 275:36781-36786(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.
RC TISSUE=Leukocyte;
RX MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
RT "Molecular cloning and characterization of a new human histamine
receptor, HRH4";
Biochem. Biophys. Res. Commun. 279:615-620(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Jones P.G., Wu S., Betty M.;
RT "Cloning of a novel histamine receptor";
Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR008102; Histamin_H4_rcpt.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_FL_2; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_FL_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 390 AA; 44463 MW; 334F219F33F209AD CRC64;

Query Match 66.3%; Score 1357.5; DB 2; Length 390;
Best Local Similarity 67.6%; Pred. No. 1.3e-89;
Matches 265; Conservative 42; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
DB 1 MPDINSTINLSRITLAFMSSLAFALMGNVILAFVVDKRLRHSRYFFLNLAIS 60

QY 61 DFLVGLISIPLYIPHLVFNWFGGICMFWLITDYLLCTASVNVILISDYRYSQSVNAV 120
DB 61 DFFVGVISIPLYIPHLVFNWFGGICMFWLITDYLLCTASVNVILISDYRYSQSVNAV 120

QY 121 SYRAQHTGIMKIQAQVAVVILAFVNGPMLASDSKNSNTKDCBPGFVTEWYILTIT 180
DB 121 SYRQHTGILKIVLMVAVVILAFVNGPMLILVSETWKDEGS--ECBPGFSEWYIVAIT 178

QY 181 MLLEFLLPVISVAVFNVQIYWSLWKRLSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFLIPVILVAVFNNIYWSLWKRDHLSRCQSHPGTAVSSNCSQSPRCGLSSRGSL 238

QY 241 PGLKESAAHSRSPRRKSSILVLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILLRG 300
DB 239 SASTEMVSLHSEQRKRLSLMTSLRTKMSNRISAKSGSFSQSDSVGLQRHAEALLRA 298

QY 301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPF 360
DB 299 RLAKSLAILLGVFAVCWAPYSLFTIVLSFYSETGSKSVWYIAFWLQWNSFVNPF 358

QY 361 PLCHRRFQKAFWKILCVTKWPALS-QNQSVSS 391
DB 359 PLCHKRFQKAFKIFCIIKQPLSPHSRVS 390

RESULT 8
Q8NV9_PIG
ID Q8NV9_PIG PRELIMINARY; PRT; 390 AA.
AC Q8NV9;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 21-FEB-2006, entry version 19.
DE Histamine H4 receptor.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;
RA Oda T., Matsumoto S., Masuno Y., Takasaki J., Matsumoto M.,
RA Kamohara M., Saito T., Ohishi T., Soga T., Hiya H., Matsushima H.,
RA Furuichi K.;
RT "cDNA cloning and characterization of porcine histamine H4 receptor.";
RL Biochim. Biophys. Acta 1575:135-138(2002).
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

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CC -----
DR EMBL; AB053300; BAB83078.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR008102; Histamin_H4_rcpt.
DR PANTHER; PTHR19266:SF82; Histaminrecept_H4; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_FL_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;

Query Match 64.0%; Score 1311.5; DB 2; Length 390;
Best Local Similarity 65.9%; Pred. No. 2.7e-85;
Matches 259; Conservative 33; Mismatches 96; Indels 5; Gaps 3;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAIMVGNVILAFVVDNRNLRHRSNYFFLNLA 58
DB 1 MSAINDTNTPLNTRIALAFMSSLALVILMGNVILAFVVDKRLRHSRYFFLNLA 60

QY 59 ISDFLVGLISIPLYIPHLVFNWFGGICMFWLITDYLLCTASVNVILISDYRYSQSVN 118
DB 61 ISDFVGVISIPLYIPHLVFNWFGGICMFWLITDYLLCTASVNVILISDYRYSQSVN 120

QY 119 AVSYRAQHTGIMKIQAQVAVVILAFVNGPMLASDSKNSNTKDCBPGFVTEWYILT 178
DB 121 AVSYRQHTGILKIVLMVAVVILAFVNGPMLVSEAWKQ--GKQCEPGLKHWVLA 178

QY 179 ITMLLEFLLPVISVAVFNVQIYWSLWKRLSRCPSHAGFSTTSSASGHLHRAGVACRT 238
DB 179 ITLFFELAPVLLVAVFNVLYWSLWKRLSRCPSHAGFSTTSSASGHLHRAGVACRT 238

QY 239 SNFGLKESAAHSRSPRRKSSILVLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILL 298
DB 239 SLSDPKESAAHSRSPRRKSSILVLRTHMNSSITAFKVGSPWRSSESAALRQREYAEILL 297

QY 299 RGRKLARSAILLSAFAICWAPYCLFTIVLSTYPTERPKSVWYSIAFWLQWNSFVNPF 358
DB 298 RARKLARSAILLGVFAICWAPYSLFTIVLSFYSETGSKSVWYIAFWLQWNSFVNPF 357

QY 359 LYPCLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
DB 358 LYPCLCHKRFQKAFKIFCIIKQPLSPHSRVS 390

RESULT 9
Q91ZY3_CAVPO
ID Q91ZY3_CAVPO PRELIMINARY; PRT; 389 AA.
AC Q91ZY3;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE Histamine H4 receptor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC -----
CC EMBL; AF358858; AAK97379.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodops.
DR InterPro; IPR008102; Histamin_H4_rcpt.
DR PANTHER; PTHR12866:SF82; Histaminerecept_H4; 1.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
SQ SEQUENCE 389 AA; 44512 MW; 51AF32FD6F1C3E4F CRC64;

Query Match 60.4%; Score 1238; DB 2; Length 389;
Best Local Similarity 62.5%; Pred. No. 5.3e-81;
Matches 245; Conservative 43; Mismatches 100; Indels 4; Gaps 3;

Qy 1 MSESNTGILPPAAQVPLAFILMSSFAFIMVGNVAVILAFVVDRLRHRNSYFFLNLAIS 60
Db 1 MLANNST-IALTSIKISITFLMSSLAITAILMGNVILAFVVDRLRHRNSYFFLNLAIA 59

Qy 61 DFLVGLISIPYIYHVLNPNFGGICMFWLITDYLLCTASVYVILSYDRYQSVSNV 120
Db 60 DFFVGAIAIPLYIPSSLYTSGKQACFWLITDYLLCTASVYVILSYDRYQSVSNV 119

Qy 121 SYRAQHTGIMKIQAQVAVVILAFVNGPMLIADSKMNSNTKDCPGFVTEWYILIT 180
Db 120 WYRAQSGTGWKIATQMAVILFSPWNGPMLIADSKMNSNTKDCPGFVTEWYILIT 177

Qy 181 MLLEFLPLVSVAYFNVQIYWSLWKRRALSCPSHAGF-STTSSSASGHLHRAGVACRTS 239
Db 178 SLLEFLPILLVAVFSAHYWSLWKREKSLRCLSHPLVPSDSSSDHGSCRPDPSRAT 237

Qy 240 NPGKESAASSHSSPRKSKILSVLRTHMNSITAFKVGFWFSESAALRQREYAEALLR 299
Db 238 LPARKETTSAGLSDKSRKSKLLFSIRAYKNSVIAKMGFLSHSDSLALQOREHIELR 297

Qy 300 GRKLARSIALLSAFLCAWAPYCLFTIVLSTYPRTERPKSVYVSIATFWLQFNFSVNPFL 359
Db 298 ARKLAKSLAILLAALFAICWAPYSLTVTIYISFFPERNLTKSTWYHTAFWLQFNFSVNPFL 357

Qy 360 YPLCHRRFQKAFWKILCVTKWPALSQNOSVSS 391
Db 358 YPLCHKRFQKAFKILPVRRQSTPPHRSIST 389

RESULT 10
QARKY3 TETNG
ID QARKY3 TETNG PRELIMINARY; PRT; 414 AA.
AC QARKY3
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE Chromosome 1 SCAP15025, whole genome shotgun sequence. (Fragment).
GN ORFNames=gSTENG0032735001;
CN Tetraodon nigroviridis (Green puffer).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.

PubMed=15496914; DOI=10.1038/nature03025;
RA Jallou O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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CC -----
CC EMBL; CAAE01015025; CAG10949.1; -; Genomic DNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004872; F: histamine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodops.
DR InterPro; IPR003980; H3_rcpt.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
FT NON TER 414 414
SQ SEQUENCE 414 AA; 46481 MW; 425E1F83C1DE28C4 CRC64;

Query Match 35.8%; Score 733.5; DB 2; Length 414;
Best Local Similarity 39.7%; Pred. No. 1.3e-44;
Matches 167; Conservative 60; Mismatches 129; Indels 65; Gaps 11;

Qy 1 MSESNTGILPPAA-----QVPLAFILMSSFAFIMVGNVAVILAFVVDRLRHR 49
Db 5 MLESNSGNLTPAVSEAGTALPGVLSVILSVLVVVVAGNALVIAFVMDKLRNQ 64

Qy 50 SNYPFLNLAISDFLVGLISIPYIYHVLNPNFGGICMFWLITDYLLCTASVYVIL 108
Db 65 SNYPFLNLAISDFLVGLISIPYIYHVLNPNFGGICMFWLITDYLLCTASVYVIL 124

Qy 109 SYDRYQSVSNVSYRAQHTGIMKIQAQVAVVILAFVNGPMLIADSKMNSNTKDC 166
Db 125 SYDRFLSVTRAVKYRVQRNMTRQAVLKKVAVVILAFVNGPMLIADSKMNSNTKDC 184

Qy 167 EPGFVTEWYILITITMLLEFLPLVSVAYFNVQIYWSLWKR-----RALSRC 212
Db 185 YAEFYFTWYLLSGSIFEFPTFVSVAFNLISYILNHRRIKOGASGDDARQGVSKK 244

Qy 213 PSHAGFTSTSSASGHLHRAGVACRTSNPGL-----KESAASSHSSPRKSKILSVLR 266
Db 245 PRDGVVTVF-----FMKTRKVC--SEPTAISAVIEDDEAPSHSSRDPNSSQLLI--- 294

NUCLEOTIDE SEQUENCE.

various isoforms are mainly coexpressed in brain, but their relative expression level varies in a region-specific manner. Isoform 3 and isoform 7 are highly expressed in the thalamus, caudate nucleus and cerebellum while isoform 5 and isoform 6 show a poor expression. Isoform 5 and isoform 6 show a high expression in the amygdala, substantia nigra, cerebral cortex and hypothalamus. Isoform 7 is not found in hypothalamus or substantia nigra.

!- MISCELLANEOUS: Does not bind to cimetidine and tripolidine. Shows modest affinity for thiopramide, imetit, N-alpha-methylhistamine and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to idopropoxyfan while isoforms 1 and 3 bind it with high affinity.

!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL; AF140538; AAD38151.1; -; mRNA.
EMBL; AB045369; BAB20090.1; -; mRNA.
EMBL; AB019000; BAB17030.1; -; mRNA.
EMBL; AJ296652; CAC51025.1; -; Genomic_DNA.
EMBL; AJ278250; CAC39434.1; -; Genomic_DNA.
EMBL; AF363791; AAK50040.1; -; mRNA.
EMBL; AL078633; CAC04014.1; -; Genomic_DNA.
EMBL; BC096840; AAH96840.1; -; mRNA.
Ensembl; ENSG00000101180; Homo sapiens.
HGNC; HGNC:5184; HRH3.
MIM; 604525; gene.
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0005886; C: plasma membrane; TAS.
GO; GO:0004969; F: histamine receptor activity; TAS.
GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. .; TAS.
GO; GO:0007269; P: neurotransmitter secretion; TAS.
InterPro; IPR000276; GPCR_Rhodopsn.
InterPro; IPR003980; H3 rcpt.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCR_RHODOPSIN.
PRINTS; PR01471; HISTAMINEHR3.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein; Membrane; Polymorphism; Receptor; Transducer; Transmembrane.

CHAIN 1 445
FT TOPO_DOM 1 39 Extracellular (Potential).
FT TRANSMEM 40 60 Potential.
FT TOPO_DOM 61 70 Cytoplasmic (Potential).
FT TRANSMEM 71 91 Potential.
FT TOPO_DOM 92 108 Extracellular (Potential).
FT TRANSMEM 109 129 Potential.
FT TOPO_DOM 130 156 Cytoplasmic (Potential).
FT TRANSMEM 157 177 Potential.
FT TOPO_DOM 178 196 Extracellular (Potential).
FT TRANSMEM 197 217 Potential.
FT TOPO_DOM 218 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT TOPO_DOM 381 395 Extracellular (Potential).
FT TRANSMEM 396 416 Potential.
FT TOPO_DOM 417 445 Cytoplasmic (Potential).
FT COMPBTAS 20 23 Poly-Ala.
FT COMPBTAS 250 256 Poly-Pro.
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT VARSPPLIC 85 98 Missing (in isoform 4).
FT VARSPPLIC 197 315 Missing (in isoform 5).
FT VARSPPLIC 227 342 Missing (in isoform 6).
FT VARSPPLIC 35.3%; Score 722.5; DB 1; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.5e-44;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFIMSSFAFMVGNVAVILAFVVDRLNLRHSNFFFLNLAIISDFLVGLIPIPIPHVL 77
DB 37 LAALMALLIVATVIGNALVWLAFVADSLRTQNNFFLLNLAIISDFLVGAFCIPLVYPVL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVNVNVLISYDRYOSVSNVSYRAQHTGIMKIQAQM 136
DB 97 TGRWTFGRGLCKLWLVVDYLLCTSAFNVLISYDRFLSVTRVSYRAQOQDTRAVRKM 156
QY 137 VAVWILAPLVNPGMILASDSWK-----NSTWKDCPEGFVTEWYILITIMLEFLPLVIS 191
DB 157 LLVWVLAFLVGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFPPLS 213
QY 192 VAYFNVIQY-----WSLWKRALSRCPSH 215
DB 214 VTFFNLSIYLNRIORTRLRDLGAREAAAGPEPPPEAQPSPPPPCGCMQKGHEAMPLH 273
QY 216 -----AGFSTTSSAGHLHRAGVACVTSNPKLESAAHSRSESPRRKSSILV 263
DB 274 RYGVGEAAVGAEGENTLGGGGG-----GSVASPTSSG-----SSRGTETPR 318
QY 264 SLRTHMNSSITAFKVSFMRSESAAALRQR-----EYAEELRGRKLARSLAILLSAF 314
DB 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFQRFELSRDRKVAKSLAVIVSIF 367
QY 315 AICWAPYCLFTIVLSTYPTPTPKSVVSYIAFWLQWNSFVNPLYPLCHRRFQKAFWKI 374
DB 368 GLCWAPYTLMIIRAACHGCVF-DYWYETSFLLWANSVNPVLYPLCHHSFRAPTKL 426
QY 375 LCVTNK 379
DB 427 LCPOK 431

RESULT 12
Q548M6_HUMAN
ID Q548M6_HUMAN PRELIMINARY; PRT; 445 AA.
AC Q548M6;
DT 24-MAY-2005, integrated into UniProtKB/TREMBL.
DT 21-FEB-2006, sequence version 1.
DT 21-FEB-2006, entry version 10.
DE Histamine H3 receptor isoform 1.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCB1_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor."
RL Neuropharmacology 0:0-0(2002).
CC !- SUBCELLULAR LOCATION: Membrane (By similarity).
CC !- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AF321910; AAL71911.1; -; mRNA.
CC Ensembl; ENSG00000101180; Homo sapiens.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004969; F: histamine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR003980; H3_rcpt.


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DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PR01471; HISTAMINEH3.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
  Transmembrane.
SQ SEQUENCE 445 AA; 48657 MW; 001205D765B705P5 CRC64;

Query Match          35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.5e-44;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFIMSSFAFAMVGNVILAFVVDNRHRSNRYFFLNLAISDFLVGLGISIPLYIPHL 77
DB 37 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLLNLAISDFLVGFCIPLYVPVL 96

QY 78 F-NNFSGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVNAVSVRAQHTGIMKIVAQM 136
DB 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQQGDTERRVRKM 156

QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPFGFTWYILITMLLEFLLPVIS 191
DB 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213

QY 192 VAYFNVOIY-----WSLWKRRALSRCPSH 215
DB 214 VTFNLSIYLNQIRRTFLRDGAREAGPDPPEAQPSPPPPGCWCKWGKGHEAMPLH 273

QY 216 -----AGFSTSSASGHLHRAGVACRTSNPGLKESAAHSRSPRRKGSILV 263
DB 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG---SSSRGTERPR----- 318

QY 264 SLRTHMNSSITAFKVGFWSESAALRQ-----EYAEILRGRKLARSAILLSAF 314
DB 319 -----SLKRGSKPSASSASLEKRMKMSQSFQRFSLSRDRKVAKSIAVVISIF 367

QY 315 AICWAPYCLFIVLSTVPRTERPKSVNYSIAFWLQWNSFVNPLYPLCHRRRQKAFWKI 374
DB 368 GLCWAPYLLMIIRAACHGCHVP-DYWTETFWLLWANSVNVPLYPLCHHHSFRAPTKL 426

QY 375 LCVTK 379
DB 427 LCPQK 431

RESULT 13
ID_HRH3_CAVPO STANDARD; PRT; 445 AA.
AC Q9J135; Q9J136;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
DT 16-NOV-2001, sequence version 2.
DT 07-MAR-2006, entry version 32.
DE Histamine H3 receptor (HRH3).
GN Names=HRH3;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS LONG AND SHORT).
RC TISSUE=Brain;
RX MEDLINE=20218440; PubMed=10757514;
RA Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,
RA Cochois V., Schwartz J.-C., Arrang J.-M.;
RT "Cloning and cerebral expression of the guinea pig histamine H3
RT receptor: evidence for two isoforms.";
RL NeuroReport 11:755-759(2000).
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylylate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of

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agonist).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; Synonyms=H3L;
CC IsoId=Q9J135-1; Sequence=Displayed;
CC Name=Short; Synonyms=H3S;
CC IsoId=Q9J135-2; Sequence=VSP_001880;
CC -!- TISSUE SPECIFICITY: Expressed widely and abundantly throughout the
CC brain. Highly expressed in discrete neuronal populations such as
CC pyramidal cells in cerebral cortex or cerebellar Purkinje cells.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AF267537; AAF78947.1; -; mRNA.
CC EMBL; AF267538; AAF78950.1; -; mRNA.
CC InterPro; IPR000276; GPCR_Rhodpan.
CC InterPro; IPR003980; H3_rcpt.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PRINTS; PR01471; HISTAMINEH3.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
  Membrane; Receptor; Transducer; Transmembrane.
KW Histamine H3 receptor.
FT CHAIN 1 445 /FTId=PRO_0000089689.
FT TOPO_DOM 1 40 Extracellular (Potential).
FT TRANSMEM 41 61 Potential.
FT TOPO_DOM 62 71 Cytoplasmic (Potential).
FT TRANSMEM 72 92 Potential.
FT TOPO_DOM 93 109 Extracellular (Potential).
FT TRANSMEM 110 130 Potential.
FT TOPO_DOM 131 157 Cytoplasmic (Potential).
FT TRANSMEM 158 178 Potential.
FT TOPO_DOM 179 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT TOPO_DOM 219 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT TOPO_DOM 381 398 Extracellular (Potential).
FT TRANSMEM 399 419 Potential.
FT TOPO_DOM 420 445 Cytoplasmic (Potential).
FT COMPLETAS 20 24 Poly-Ala.
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 276 305 Missing (in isoform Short).
FT SEQUENCE 445 AA; 48735 MW; BAE206A3887189A0 CRC64;

Query Match          35.2%; Score 721; DB 1; Length 445;
Best Local Similarity 39.8%; Pred. No. 1.1e-43;
Matches 162; Conservative 54; Mismatches 133; Indels 58; Gaps 9;

QY 18 LAFIMSSFAFAMVGNVILAFVVDNRHRSNRYFFLNLAISDFLVGLGISIPLYIPHL 77
DB 38 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLLNLAISDFLVGFCIPLYVPVL 97

QY 78 F-NNFSGSGICMFWLITDYLLCTASVNVNVLISYDRYQSVNAVSVRAQHTGIMKIVAQM 136
DB 98 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQQGDTERRVRKM 157

QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPFGFTWYILITMLLEFLLPVIS 191
DB 158 VLWVWLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 214

QY 192 VAYFNVOIY-----WSLWKRRALSRCPS 214
DB 215 VTFNLSIYLNQIRRTFLRDGAREAGPDPPEAQPSPPPPGCWCKWGKGESMPL 274

QY 215 HA-GFSTTSSSA-SGHLHRAGVACRTSNPGLKESAAHSRSPRRKGSILVSLRTHMNSS 272
DB 275 HRYGVGEAGPGEAGEAALGGSGAAASPTSSSGSSSRGTERPR-----SLKRGSKPS 327

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Qy 273 ITAFKVGSPWRSSEAAALRORAYEALLRGRKLARSALILLSAPALCWAPYCLFTTIVLSTYP 332
Db 328 ASSASLEKRMKMSQSTQR--FRLSRDKKVAKSALIIVSIFGLCWAPYTLIIIRAACH 385
Qy 333 RTEPKSVWTSIAFWLQFNSFVNPELYPLCHRRFQKAFWKILCVTK 379
Db 386 GHCVP-DYWTETSWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQK 431

RESULT 14
Q865E1 MACMU
ID Q865E1 MACMU PRELIMINARY; PRT; 445 AA.
AC Q865E1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 21-FEB-2006, entry version 15.
DE Histamine receptor H3.
GN Name=HRH3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yao B.B., Sharma R., Cassar S., Esbenshade T.A., Hancock A.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC
CC EMBL: AY231164; AAC63757.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004969; F:histamine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003980; H3_rept.
DR Pfam: PF00001; 7tm.1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 445 AA; 48591 MW; E79440A4EC09CA8C CRC64;

Query Match 35.18; Score 718.5; DB 2; Length 445;
Best Local Similarity 38.78; Pred. No. 1.7e-43;
Matches 163; Conservative 52; Mismatches 121; Indels 85; Gaps 9;

Qy 18 LAFIMSSFAIMVGNWAVILAFVVDNLRHRSNYFFLNLAISDFLVGLISIPLYPHVL 77
Db 37 LAALMALLIVATVIGNALVWALFVADSSLRQNNFLLNLAISDFLVGACIPLYPVYL 96
Qy 78 F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNVSYRAQHTGIMKIYAQM 136
Db 97 TGRWTFGRGLKLVWVYLLCTSSAFNVLISYDRFLSVTRAVSYRAQGNTRAVRKM 156
Qy 137 VAWVILAFVNGPMILASDSWK-----NSTNTKDCBGFTEWYILTITMLLFFLPVIS 191
Db 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFNYFWYFLITASTLEFFTPFLS 213
Qy 192 VAFNVVOIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLIQRTLRLDGAREAGGPPPPPAQSPPPPPCGCWCQKQHGHEAMPLH 273
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Qy 216 -----AGFTSTSSASGHLHRGAVACRTSNPGLKESAAHRHSESPRRKSSILVSLRT 267
Db 274 RYGVGEAAAAGAEATALGGGGGSAASPTSSG-----SSSRGTERPR----- 318
Qy 268 HMSNSTAFKVGSPWRSSEAAALROR-----EYAEALLRGRKLARSALILLSAPALCW 318
Db 319 -----SLKSGSKPSASSASLEKRMKMSQSTQRFLSRDKKVAKSALIIVSIFGLCW 371
Qy 319 APYCLFTTIVLSTYPTERTPKSVWTSIAFWLQFNSFVNPELYPLCHRRFQKAFWKILCVT 378
Db 372 APYTLIIIRAACHGHCVP-DYWTETSWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQK 430
Qy 379 K 379
Db 431 K 431

RESULT 15
HRH3 RAT
ID -HRH3 RAT STANDARD; PRT; 445 AA.
AC Q9QYN8; Q9QYN6; Q9QYN7; Q9QYN9;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-2000, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Histamine H3 receptor (HRH3).
GN Name=Hrh3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC TISSUE=Hypothalamus;
RX MEDLINE=20330707; PubMed=10869375;
RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
RT "Cloning of rat histamine H3 receptor reveals distinct species
RT pharmacological profiles.";
RL J. Pharmacol. Exp. Ther. 293:771-778 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
RC TISSUE=Corpus striatum;
RX MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
RA Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
RT "High constitutive activity of native H3 receptors regulates histamine
RT neurons in brain.";
RL Nature 408:860-864 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1; 2; 3 AND 4).
RA Itadani H., Takimura T., Nakamura T., Ohta M.;
RT "Cloning of a novel G protein-coupled receptor.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huvav A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3
RT receptor.";
RL Mol. Pharmacol. 55:1101-1107 (1999).
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -1- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylylate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
CC agonist).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=H3L;
CC IsoId=Q9QYN8-1; Sequence=displayed;
CC Name=2; Synonyms=H3S;
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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:34:45 ; Search time 29 Seconds
(without alignments)
1180.154 Million cell updates/sec

Title: US-10-626-445-8

Perfect score: 2048

Sequence: 1 MSENSTGILPPAAQVPLAF.....WKILCVTKWALPSONQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents AA.*
- 1: /EMC_Celerra_SIDS3/protodata/2/iaa/5_COMB.pep.*
 - 2: /EMC_Celerra_SIDS3/protodata/2/iaa/6_COMB.pep.*
 - 3: /EMC_Celerra_SIDS3/protodata/2/iaa/7_COMB.pep.*
 - 4: /EMC_Celerra_SIDS3/protodata/2/iaa/H_COMB.pep.*
 - 5: /EMC_Celerra_SIDS3/protodata/2/iaa/PTUS_COMB.pep.*
 - 6: /EMC_Celerra_SIDS3/protodata/2/iaa/RE_COMB.pep.*
 - 7: /EMC_Celerra_SIDS3/protodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1370.5	66.9	390	2	US-09-414-010-2
2	1370.5	66.9	390	2	US-09-812-216-2
3	1370.5	66.9	390	2	US-09-875-076-14
4	722.5	35.3	445	1	US-08-985-090-2
5	722.5	35.3	445	2	US-09-165-543-2
6	722.5	35.3	445	2	US-09-167-354-7
7	722.5	35.3	445	2	US-09-642-855-7
8	722.5	35.3	445	2	US-09-642-514-7
9	722.5	35.3	445	2	US-09-642-852-7
10	722.5	35.3	445	2	US-10-453-106-1
11	722.5	35.3	449	2	US-09-949-016-10930
12	722.5	35.3	453	2	US-09-891-053-20
13	718.5	35.1	445	2	US-10-453-106-2
14	716.5	35.0	445	2	US-09-165-543-5
15	716.5	35.0	445	2	US-09-891-053-25
16	716.5	35.0	445	2	US-10-453-106-3
17	709.5	34.6	413	2	US-09-891-053-1
18	621.5	30.3	351	2	US-09-524-162-2
19	582.5	28.4	362	1	US-08-985-090-5
20	582.5	28.4	362	2	US-09-165-543-32
21	427	20.8	348	1	US-08-118-270-13
22	427	20.8	348	5	PCT-US93-08528-13
23	427	20.8	355	1	US-08-118-270-11
24	427	20.8	355	5	PCT-US93-08528-11
25	415.5	20.3	479	1	US-08-313-553-7
26	415.5	20.3	479	2	US-08-767-993-7

27	408	19.9	460	2	US-09-826-509-513	Sequence 513, App
28	402.5	19.7	590	2	US-09-538-092-367	Sequence 967, App
29	399.5	19.5	532	2	US-09-826-509-521	Sequence 521, App
30	397.5	19.4	590	2	US-09-826-509-517	Sequence 517, App
31	393	19.2	354	1	US-08-313-853-9	Sequence 9, Appli
32	393	19.2	354	2	US-08-767-993-9	Sequence 9, Appli
33	390.5	19.1	501	1	US-08-722-001-14	Sequence 14, Appli
34	390.5	19.1	501	1	US-08-467-568-9	Sequence 9, Appli
35	390.5	19.1	501	1	US-09-030-582-9	Sequence 9, Appli
36	389.5	19.0	513	1	US-08-406-855A-21	Sequence 21, Appli
37	389.5	19.0	513	2	US-09-206-899-21	Sequence 21, Appli
38	389.5	19.0	515	1	US-08-444-734A-7	Sequence 7, Appli
39	389.5	19.0	515	1	US-08-406-855A-22	Sequence 22, Appli
40	389.5	19.0	515	2	US-09-206-899-22	Sequence 22, Appli
41	388.5	19.0	400	2	US-09-826-509-491	Sequence 491, App
42	388.5	19.0	572	1	US-08-334-698-2	Sequence 2, Appli
43	388.5	19.0	572	1	US-08-228-932-2	Sequence 2, Appli
44	388.5	19.0	572	1	US-08-468-939-2	Sequence 2, Appli
45	388.5	19.0	572	1	US-08-722-001-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-010-2

Query Match	66.9%	Score 1370.5;	DB 2;	Length 390;
Best Local Similarity	68.1%	Pred. No. 2e+105;		
Matches	267;	Conservative	40;	Mismatches 82;
			Indels	3;
			Gaps	2;
Qy	1	MSENSTGILPPAAQVPLAFIMSSFAFIMVGNAAVILAFVVDRLHRHSNYFFNLAIS	60	
Db	1	MDPTNSTINLSLSTRVTLAFMSLVAFIMGNALVILAFVVDKRLHRSSYFFNLAIS	60	
Qy	61	DFLVGLISILPIYIPHLFNNFGSGICMFWLITDYLCTASVYNNIVLISYDRYSVSNV	120	
Db	61	DFVGVVISILPIYIPHTLFEWDFGKEICVFWLITDYLCTASVYNNIVLISYDRYSVSNV	120	
Qy	121	SYRAQHTGIMKIQAQVAVVILAFVNGPMILASDSKWNSTNTKDCPGFTWYILIT	180	
Db	121	SYRTQHTGVILKIVTLAVVAVVILAFVNGPMILVSESWKDEGS--ECEPGFTSEWYILAIT	178	
Qy	181	MLLEFLPLVLSVAFVNOIVKSLWKRLALSRCPSHAGFTTSSASGHLHAGVACRTSN	240	
Db	179	SFLSEFVPIVLVAVFNNIIVSLWKRLHRCQHPGLTVSSNICGHSFGRLSRRSL	238	
Qy	241	PGLKESAAARHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSEAAALRQRYAELRG	300	
Db	239	SASTEVPAFHSERQRKSSILMFSSRTKMSNTTASKMGSPSQSDSVALHQHREVELLRA	298	
Qy	301	RKLARSAILLSAPACWAPCYCLFTIVLSTYPTPTPKSVWVYSIAFWLQWNSFVNPLY	360	

Db 299 RRLAKSLAIIIGVAVCWAPYSLFTIVLSFYSGATGPKSVYVIAFWLQWFNFSVNPPLY 358
Qy 361 PLCHRRFQKAFWKILCVTKKPALSO-NQSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKKPALSO-NQSVSS 390

RESULT 2

US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 66.9%; Score 1370.5; DB 2; Length 390;
Best Local Similarity 68.1%; Pred. No. 2e-105;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSESNSGILPPAAQVPLAFMSSFAFIMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLAFMSSLVAFVAFIMGNALVILAFVVDKRLRHSYFFLNLAIS 60
Qy 61 DFLVGLISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVNVNVLISYDRYQSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVNVNVLISYDRYQSVSNV 120
Qy 121 SYRAQHTGIMKIQAQVAVMILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVLAFVNGPMLVSESWKDEGS--ECEPFGFFSEWYILIT 178
Qy 181 MLLEFLLPVTSVAVFNVQIYWSLWKRALSRCPHAGFTSTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVTLVAFVNNVNIWSLWKRLSRCPHAGFTSTSSASGHLHRAGVACRTSN 238
Qy 241 PGLKESAAHRHSESPRKSSILVSLRTHMNSSITAFKVGFSFWRSESAAALRQREYAEILRG 300
Db 239 SASTEVPAFPHSERQRRKSSLMFSRTHMNSTTASKMGFSQSDSVALLHQREHVELLRA 298
Qy 301 RKLARSLAIIISAFACWAPYCLFTIVLSTYPRTERPKSVWYSYAFWLNQWPNFSVNPPLY 360
Db 299 RRLAKSLAIIIGVAVCWAPYSLFTIVLSFYSGATGPKSVYVIAFWLQWFNFSVNPPLY 358
Qy 361 PLCHRRFQKAFWKILCVTKKPALSO-NQSVSS 391
Db 359 PLCHRRFQKAFWKILCVTKKPALSO-NQSVSS 390

RESULT 3

US-09-875-076-14
; Sequence 14, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huong T.
; APPLICANT: Liao, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 66.9%; Score 1370.5; DB 2; Length 390;

Best Local Similarity 68.1%; Pred. No. 2e-105;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

Qy 1 MSESNSGILPPAAQVPLAFMSSFAFIMVGNVAVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db 1 MPDTNSTINLSLSTRVTLAFMSSLVAFVAFIMGNALVILAFVVDKRLRHSYFFLNLAIS 60
Qy 61 DFLVGLISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVNVNVLISYDRYQSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVNVNVLISYDRYQSVSNV 120
Qy 121 SYRAQHTGIMKIQAQVAVMILAFVNGPMLASDSWKNSTNTKDCBPGFVTEWYILIT 180
Db 121 SYRTQHTGVLKIVTLMAVAVLAFVNGPMLVSESWKDEGS--ECEPFGFFSEWYILIT 178

QY 181 MLLBFLPVLISVAVNQIYKSLMKRALSRCPHAGSTTSSASGHLHRAGVACRTSN 240
Db 179 SFLEFVPIVILVAVFNMMIYKSLWKDHLSCQHPGLTAVSSNICGHSFGRSLSRSL 238
QY 241 PGLKESAAHSRHSPPRRKSSILVSLRTHMNSSITAFKVGSEFWRSESAAALRQREVAELLRG 300
Db 239 SASTEVPASHSERQRRKSSLMFSRYKMSNTTASRKGSEFQSDSVALHQREHVELLRA 298
QY 301 RKLARSAILLSAPAIWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWPNFSVNPFLY 360
Db 299 RRLAKSAILLGVPAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWPNFSVNPFLY 358
QY 361 PLCHRRFQKAFKWLICVTKMPALSO-NOSVSS 391
Db 359 PLCHRRFQKAFKWLICVTKMPALSO-NOSVSS 390

RESULT 4
US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5885693
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS,
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-2

Query Match 35.3%; Score 722.5; DB 1; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSFAPAIMVGNVILAFVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLNLAISDFLVGAFCIPLYVPYL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVYNIIVLSYDRYQSVNSVRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGCKLWVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWWILAFVNGPMILASDSWK-----NSNTKDCSPGFTEWYILTITMLLEFLPVIS 191
Db 157 LLVWVLAFLDYGPAIL---SWEYLSGSGSIPEGHCYAEFFYNNYFLITASTLEFFTPFLS 213

QY 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215
Db 214 VTFENLSIYLNIRRLDGAEEAAGBPPEAQPSPPPPPGCGWCKGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACHTSNPGLKESAAHSRHSPPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG-----GSVASPTSSG-----SSSRGTERPR 318
QY 264 SLRTHMNSSITAFKVGSEFWRSESAAALRQREVAELLRGRKLARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKMKMWVSQSTQRFRLSRDRKVAKSLAVIVSIF 367
QY 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWPNFSVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYTLMLIIRAACHGCV-P-DYWYETSFLLWANSVNPVLYPLCHHSFRFAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 5
US-09-165-543-2
; Sequence 2, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-2

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSFAPAIMVGNVILAFVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSSLTQNNFFLNLAISDFLVGAFCIPLYVPYL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVYNIIVLSYDRYQSVNSVRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGCKLWVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWWILAFVNGPMILASDSWK-----NSNTKDCSPGFTEWYILTITMLLEFLPVIS 191
Db 157 LLVWVLAFLDYGPAIL---SWEYLSGSGSIPEGHCYAEFFYNNYFLITASTLEFFTPFLS 213

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Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLEFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VAFNVQIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRLRLDGAAREAGPEPPPEAQPSPPPGCGWCKWGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRSHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG-----SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAEILRGKRLARSAILLSAF 314
Db 319 -----SLKRGSKPSASASLEKRMKMWVSQSFQRFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSFVNPFLYPLCHRRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLPCLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 6
US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-167-354-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSPFAIMVGNVLAFAVDNLRHRSNYFNLAIISDFLVGLISIPLYIHPVL 77
Db 37 LAALMALLIVATVLGNALVMAFVADSSLRTONNFFLLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVNVNVLISYDRYQSVSNVSVRAOQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLEFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VAFNVQIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRLRLDGAAREAGPEPPPEAQPSPPPGCGWCKWGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRSHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG-----SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAEILRGKRLARSAILLSAF 314
Db 319 -----SLKRGSKPSASASLEKRMKMWVSQSFQRFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSFVNPFLYPLCHRRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLPCLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 7
US-09-642-855-7
; Sequence 7, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-642-855-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSPFAIMVGNVLAFAVDNLRHRSNYFNLAIISDFLVGLISIPLYIHPVL 77
Db 37 LAALMALLIVATVLGNALVMAFVADSSLRTONNFFLLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVNVNVLISYDRYQSVSNVSVRAOQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLEFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VAFNVQIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRLRLDGAAREAGPEPPPEAQPSPPPGCGWCKWGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRSHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG-----SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAEILRGKRLARSAILLSAF 314
Db 319 -----SLKRGSKPSASASLEKRMKMWVSQSFQRFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSFVNPFLYPLCHRRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLPCLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431
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Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG-----SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAEILRGKRLARSAILLSAF 314
Db 319 -----SLKRGSKPSASASLEKRMKMWVSQSFQRFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSFVNPFLYPLCHRRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLPCLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 7
US-09-642-855-7
; Sequence 7, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-642-855-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFMSPFAIMVGNVLAFAVDNLRHRSNYFNLAIISDFLVGLISIPLYIHPVL 77
Db 37 LAALMALLIVATVLGNALVMAFVADSSLRTONNFFLLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NNFGSGICMFWLITDYLCTASVNVNVLISYDRYQSVSNVSVRAOQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKM 156
QY 137 VAWMILAFVNGPMILASDSWK-----NSTNTKDCBPGFVTEWYILITMLLEFLPLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VAFNVQIY-----WSLWKRRALSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRLRLDGAAREAGPEPPPEAQPSPPPGCGWCKWGHEAMPLH 273
QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHRSHSPRRKSSILV 263
Db 274 RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSG-----SSRGTERRP- 318
QY 264 SLRTHNSSITAFKVGSWFRSESAALRQR-----EYAEILRGKRLARSAILLSAF 314
Db 319 -----SLKRGSKPSASASLEKRMKMWVSQSFQRFRLSRDRKVAKSIAVIVSIF 367
QY 315 AICWAPCYCLFTIVLSTYPRTERPKSVWYSIAFWLQFNFSFVNPFLYPLCHRRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGCHVP-DYWYETSFLLWANSVNPVLPCLCHHSFRRAFTKL 426
QY 375 LCVTK 379
Db 427 LCPQK 431
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QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 8
US-09-642-514-7
; Sequence 7, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-514-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFLMSSFAFALMGVAVVILAFVVDRLNRHRSYFFLNLAISDFLVGLISPLYPHVL 77
Db 37 LAALMALLIVATVLGNALVMLAFVADSLRTQNNFFLNLAISDFLVGAFICPLYPVYL 96

QY 78 F-NNFGSGICMFWLITDYLLCTASVNVILISYDRVQSVNAVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSAFNIVLISYDRFLSVTRAVSYRAQQDTRRAVRKM 156

QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPGFVTEWYILITITMLLEFLLPVIS 191
Db 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNNWYFLITASTLEFFTPFLS 213

QY 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215
Db 214 VTFFNLSTIYLNRIQRTRLRLDGAEEAGPEPPPEAQPSPPPPGCGWQKGHEAMPLH 273

QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHSRSPRKSILV 263
Db 274 RYGVGEAAVGAEEAGELTGGGGG---GSVASPTSSG-----SSSRGTERPR----- 318

QY 264 SLRTHMNSSITAFKVGFSWRSESAAALROR-----EYAEALLRGRKLARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKWSQSFTQRFELSRDRKVAKSLAVIVSIF 367

QY 315 AICWAPYCLFTIVLSTYPTERTPKSVVYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGHCV-P-DYWTYETSWLLWANSVNPVLYPLCHHSFRFAFTKL 426

QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 9
US-09-642-852-7
; Sequence 7, Application US/09642852
; Patent No. 6855560

; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-852-7

Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

QY 18 LAFLMSSFAFALMGVAVVILAFVVDRLNRHRSYFFLNLAISDFLVGLISPLYPHVL 77
Db 37 LAALMALLIVATVLGNALVMLAFVADSLRTQNNFFLNLAISDFLVGAFICPLYPVYL 96

QY 78 F-NNFGSGICMFWLITDYLLCTASVNVILISYDRVQSVNAVSYRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSAFNIVLISYDRFLSVTRAVSYRAQQDTRRAVRKM 156

QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTKDCPGFVTEWYILITITMLLEFLLPVIS 191
Db 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNNWYFLITASTLEFFTPFLS 213

QY 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215
Db 214 VTFFNLSTIYLNRIQRTRLRLDGAEEAGPEPPPEAQPSPPPPGCGWQKGHEAMPLH 273

QY 216 -----AGFSTTSSASGHLHRAGVACRTSNPGLKESAAHSRSPRKSILV 263
Db 274 RYGVGEAAVGAEEAGELTGGGGG---GSVASPTSSG-----SSSRGTERPR----- 318

QY 264 SLRTHMNSSITAFKVGFSWRSESAAALROR-----EYAEALLRGRKLARSAILLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKWSQSFTQRFELSRDRKVAKSLAVIVSIF 367

QY 315 AICWAPYCLFTIVLSTYPTERTPKSVVYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYTLMIIRAACHGHCV-P-DYWTYETSWLLWANSVNPVLYPLCHHSFRFAFTKL 426

QY 375 LCVTK 379
Db 427 LCPQK 431

RESULT 10
US-10-453-106-1
; Sequence 1, Application US/10453106
; Patent No. 6906060
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPIRROLO[1,2-A]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPIRDO[1,2-A]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPIRAZINO[1,2-A]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/10/453,106
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/387,047


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; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-453-106-1

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Query Match 35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;

Qy	18	LAFUMSSFAIMVGNVAVILAFVVDRLNRHRSYFFTLNLAISDFLVLGLISITPLIYIPHV	77
Db	37	LAALMALLIATVLGNALVMLAFVADSSLRQTQNNFFLLNLAISDFLVGAFCIPLVPVYL	96
Qy	78	F-NNFGSGICMFWLIITDYLLCTASVYVILISYDRYOSVSNVASYRAQHTGIMKIVAQ	136
Db	97	TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTVASVYRAQOGDTRAVRKM	156
Qy	137	VAVWILAFVNGPMILASDSWK-----NSTWTKDCPEGFVTEWYILTTIMLEFLLPVIS	191
Db	157	LLVWVLAFLLYGPAIL---SWEYLSGGSSIEGHCHYAEFFVYNNWYFLITASTLEPFTPLS	213
Qy	192	VAYENVVOIY-----WSLWKKRALSRCPSH	215
Db	214	VTFFNLSIYLNIOBRURLRGAREAGPEPPEAQSPPPPGCWGCKQGHGEMPLH	273
Qy	216	-----AGFTSTSSASGHLHAGVACRTSNFGLKESAAHRSHSESPRRKSSILV	263
Db	274	RYGVGEAAVGAEGEATLGGGGG---GSVASPTSSSG-----SSSRGTGRPR-----	318
Qy	264	SLRTHMNSSITAFKVGSGFSWRSESAAALROR-----EYAEILLRGRKLARSIALILLSAF	314
Db	319	-----SLKRGSKPSASSASLEKRMKWSQSFTQRFLSRDRKVAKSLAVIVISIF	367
Qy	315	AICWAPYCLFTIVLSTYPRTERPKSVWVYSIAPWLQWFNFSVFNVPFLYPLCHRRFQKAFWKI	374
Db	368	GLCWAPYTLMLIIIRAACHGHCVP-DYWTETSPWLLWANSVNNPVLYPLCHHSFRFAFTKL	426
Qy	375	LCVTK 379	
Db	427	LCPOK 431	

```

RESULT 11
US-09-949-016-10930
; Sequence 10930, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10930
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10930

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Query Match	35.3%;	Score	722.5;	DB	2;	Length	449;
Best Local Similarity	38.8%;	Prod. No.	8.9e-52;				
Matches	165;	Conservative	51;	Mismatches	116;	Indels	93;
Gaps	10;						
Qy	18	LAFIMSGFAIMVGN	AVILAFVDRNLRHRSNYFFLNLAISDFLVGLGISIPLYI	PHVL	77		
Db	41	LAALMALLIVATV	IGNALVMAFVADSSLRQTQNNFFLLNLAISDFLVGAFCIPLYVPV	L	100		
Qy	78	F-NWNPFGICMFWL	ITDYLLCTASVYVNI	VLISYDRYQSVSNVASYRAOHTGIMKI	VAQM	136	
Db	101	TGRWTFGRGCKL	WVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAOQGDTRR	AVRKM	160		
Qy	137	VAVVILAFVNGPM	ILASDSWK-----NSTNTKDCBPGFTWETILATITMLLE	FLLPV	191		
Db	161	LLVWVLAFLYGA	LL-----SWEVLSGGSSIPEGHCYAEFFVNYFLTITASTLE	FTPLS	217		
Qy	192	VAFNVQIY-----		WSLWKRALSRCP	SH	215	
Db	218	VTFNLSIYLI	QRTRLRLDGAAREAGPEPPPEAQSPPPPCWCWCQGHG	EAMPLH	277		
Qy	216	-----AGFTSTSS	ASGHLHRAGVACRTSNPGLKESAAARHSESFRK	KSILV	263		
Db	278	RYGVGEAAVGA	EAGETLGGGGG-----GSVASPTSSG-----SSRGT	ERPR	322		
Qy	264	SLRTHNMSITAP	KVGSFWKSEGAALRQ-----EYALLRGKLABSLAILLS	SAF	314		
Db	323	-----SLKRGSKP	SASSASLEKRMKWSQSFTQRPRLSRDRKVA	KSIAV	371		
Qy	315	AICWAPYCLFT	IVLSTPRTERPKSVWYSIAFWLQWFNSFVNPPLYPLCHRR	RFQAFWKI	374		
Db	372	GLCWAPYTLML	ITRAACHGHCVP-DYWYETISFWLLWANSANPVL	YPLCHHS	FRFAFTKL	430	
Qy	375	LCWTK	379				
Db	431	LCPOK	435				

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RESULT 12
US-09-891-053-20
; Sequence 20, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-053-20

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Query Match 35.3%; Score 722.5; DB 2; Length 453;
Best Local Similarity 38.8%; Pred. No. 9e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;
Ov 18 IAFIMSSPFAFATMGVGNAAVTLAFVDRNLRHRSNYFFELNLAISDFLVGLISIPYIPHL 77

Db 37 LAALMALLIVATVGLNVALVLAFAVDSSLRQNNFFLNLAISDFLVGAFCIPLYVPVYL 96
Qy 78 F-NWNFSGICMFWLITDYLCTASVYVNLISYDRYOSVSNVSYRAQHTGIMKIYAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156
Qy 137 VAVWILAFVNGPMLASDSWK-----NSTNTKDCPEGFVTEWYILITMLLEFLLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTFPLS 213
Qy 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215
Db 214 VTFNLSIYLNIOQRRLRLDGAAREAGPEPPEAQPSPPPPCGCMGCKQHGSEAMPLH 273
Qy 216 -----AGFTTSSASGHLHRAAGVACRTSNPGLKESAAASRHSESPRRKSSILV 263
Db 274 RYGVGEAAVGAEGATELGGGGG-----GSVASPTSSSG-----SSSRGTTERPR----- 318
Qy 264 SLRTHMNSSITAFKVGSWFRSESAALRQ-----EYAEALLRGRKLARSAILLSAF 314
Db 319 -----SLRGRKSPSASSASLEKRMKMWVSQSFQTRFLSRDRKVAKSLAVIVSIF 367
Qy 315 AICWAPYCLFTVILSTYRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYLLMIIRAACHGCHVP-DYWTYETSWLLWANSVNPVLYPLCHHSFRRAFTKL 426
Qy 375 LCVTK 379
Db 427 LCPQK 431

RESULT 13

US-10-453-106-2
; Sequence 2, Application US/104531106
; Patent No. 6906060
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPIRROLO [1,2-A] PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPIRIDO [1,2-A] PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPIRAZINO [1,2-A] AZEPINES
; FILE REFERENCE: 6483-200-US
; CURRENT APPLICATION NUMBER: US/10/453,106
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/387,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Monkey
US-10-453-106-2

Query Match 35.1%; Score 718.5; DB 2; Length 445;
Best Local Similarity 38.7%; Pred. No. 1.9e-51;
Matches 163; Conservative 52; Mismatches 121; Indels 85; Gaps 9;

Qy 18 LAFIMSSFAFIMVGNVAVILAFVVDNRNLRHSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVGLNVALVLAFAVDSSLRQNNFFLNLAISDFLVGAFCIPLYVPVYL 96
Qy 78 F-NWNFSGICMFWLITDYLCTASVYVNLISYDRYOSVSNVSYRAQHTGIMKIYAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAQOQDTRAVRKM 156
Qy 137 VAVWILAFVNGPMLASDSWK-----NSTNTKDCPEGFVTEWYILITMLLEFLLPVIS 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTFPLS 213

Qy 192 VAYFNVOIY-----WSLWKRRLSRCPSH 215
Db 214 VTFNLSIYLNIOQRRLRLDGAAREAGPEPPEAQPSPPPPCGCMGCKQHGSEAMPLH 273
Qy 216 -----AGFTTSSASGHLHRAAGVACRTSNPGLKESAAASRHSESPRRKSSILVSLRT 267
Db 274 RYGVGEAAVGAEGATELGGGGGSAASPTSSSG-----SSSRGTTERPR----- 318
Qy 268 HNMSSITAFKVGSWFRSESAALRQ-----EYAEALLRGRKLARSAILLSAFIACW 318
Db 319 -----SLRGRKSPSASSASLEKRMKMWVSQSFQTRFLSRDRKVAKSLAVIVSIFGLCW 371
Qy 319 APYCLFTVILSTYRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILCVT 378
Db 372 APYLLMIIRAACHGCHVP-DYWTYETSWLLWANSVNPVLYPLCHHSFRRAFTKLCPQ 430
Qy 379 K 379
Db 431 K 431

RESULT 14

US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-165-543-5

Query Match 35.0%; Score 716.5; DB 2; Length 445;
Best Local Similarity 40.2%; Pred. No. 2.8e-51;
Matches 165; Conservative 54; Mismatches 128; Indels 63; Gaps 10;

Qy 18 LAFIMSSFAFIMVGNVAVILAFVVDNRNLRHSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVGLNVALVLAFAVDSSLRQNNFFLNLAISDFLVGAFCIPLYVPVYL 96
Qy 78 F-NWNFSGICMFWLITDYLCTASVYVNLISYDRYOSVSNVSYRAQHTGIMKIYAQM 136

Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSVRAQQGDTRRAVRKM 156
Qy 137 VAVMILAFVNGPMILASDWSK-----NSTNTKDCPCGFVTEWYILITITMLLEFLLPVIS 191
Db 157 ALVWVLAFLYGGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTFPLS 213
Qy 192 VAYFNVQIYWSLWKRRAL-----SRCPSHAGFSTTTSSSASGH-----LH 230
Db 214 VTFFNLISYLNQRRTRLRLDGGREAGPEPPDPAQSPPPAPPCWGCWPKHGGEAMPLH 273
Qy 231 RAGVACTSNPGLK-----ESAAASHSESPPRKSILVSLRTHM 269
Db 274 RYGVG--EAGPGVEAGEAALGGSGGGAASPTSSSGSSSRGTERPR-----SLKRG 324
Qy 270 NSSITAFKVGSPWSESAALRQREYAEALLRGRKLARSLAILLSAFAICWAPYCLFTIVLS 329
Db 325 KPSASSASLEKRMKMWVSQSIQR--FRLSRDKKVAKSLAIIVSIFGLCWAPYTLLMIIRA 382
Qy 330 TYPRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILCVTK 379
Db 383 ACHGRCLP-DYWTYTSFWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQK 431

RESULT 15

US-09-891-053-25
; Sequence 25, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-891-053-25

Query Match 35.0%; Score 716.5; DB 2; Length 445;
Best Local Similarity 40.2%; Pred. No. 2.8e-51;
Matches 165; Conservative 54; Mismatches 128; Indels 63; Gaps 10;
Qy 18 LAFLMSSFAFAIMGVNAVILAFVVDRLNRHSNYFFLNLAISDFLVGLISIPLYIPHL 77
Db 37 LAALMALLIVATVLGNALVMAFVADSSLRQNNFFLNLAISDFLVGAFCIPLYVPVL 96
Qy 78 F-NNPFGSGICMFWLITDYLCTASVNVNVLISYDRVQSVNAVSVRAQHTGIMKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSVRAQQGDTRRAVRKM 156
Qy 137 VAVMILAFVNGPMILASDWSK-----NSTNTKDCPCGFVTEWYILITITMLLEFLLPVIS 191
Db 157 ALVWVLAFLYGGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTFPLS 213
Qy 192 VAYFNVQIYWSLWKRRAL-----SRCPSHAGFSTTTSSSASGH-----LH 230
Db 214 VTFFNLISYLNQRRTRLRLDGGREAGPEPPDPAQSPPPAPPCWGCWPKHGGEAMPLH 273

Qy 231 RAGVACTSNPGLK-----ESAAASHSESPPRKSILVSLRTHM 269
Db 274 RYGVG--EAGPGVEAGEAALGGSGGGAASPTSSSGSSSRGTERPR-----SLKRG 324
Qy 270 NSSITAFKVGSPWSESAALRQREYAEALLRGRKLARSLAILLSAFAICWAPYCLFTIVLS 329
Db 325 KPSASSASLEKRMKMWVSQSIQR--FRLSRDKKVAKSLAIIVSIFGLCWAPYTLLMIIRA 382
Qy 330 TYPRTERPKSVWYSIAFWLQWNSFVNPFLYPLCHRRFQKAFWKILCVTK 379
Db 383 ACHGRCLP-DYWTYTSFWLLWANSVNPVLYPLCHYSFRRAFTKLLCPQK 431

Search completed: May 24, 2006, 13:35:39
Job time : 30 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: May 24, 2006, 13:35:10 ; Search time 85 Seconds
(without alignments)
2130.788 Million cell updates/sec
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Perfect score: 2048
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
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3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US09_PUBCOMB.pbp.*
4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10A_PUBCOMB.pbp.*
5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10B_PUBCOMB.pbp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2048	100.0	391	5	US-10-626-126-8
3	2048	100.0	391	5	US-10-626-398-8
4	1735	84.7	391	5	US-10-626-445-9
5	1735	84.7	391	5	US-10-626-126-9
6	1735	84.7	391	5	US-10-626-398-9
7	1370.5	66.9	390	3	US-09-812-216-2
8	1370.5	66.9	390	3	US-09-910-411-2
9	1370.5	66.9	390	3	US-09-875-076-14
10	1370.5	66.9	390	3	US-09-876-252-14
11	1370.5	66.9	390	3	US-09-852-165-2
12	1370.5	66.9	390	3	US-09-891-138A-6
13	1370.5	66.9	390	4	US-10-052-193-2
14	1370.5	66.9	390	4	US-10-349-253A-2
15	1370.5	66.9	390	4	US-10-225-567A-629
16	1370.5	66.9	390	4	US-10-272-983-14
17	1370.5	66.9	390	4	US-10-354-769-2
18	1370.5	66.9	390	4	US-10-393-807-14
19	1370.5	66.9	390	4	US-10-417-820A-14
20	1370.5	66.9	390	4	US-10-696-673-2
21	1370.5	66.9	390	4	US-10-723-955-14
22	1370.5	66.9	390	4	US-10-782-596-14
23	1370.5	66.9	390	4	US-10-737-619-2
24	1370.5	66.9	390	5	US-10-626-445-2
25	1370.5	66.9	390	5	US-10-684-206-20
26	1370.5	66.9	390	5	US-10-616-088-2
27	1370.5	66.9	390	5	US-10-626-126-2

28	1370.5	66.9	390	5	US-10-626-398-2	Sequence 2, Appli
29	1370.5	66.9	390	5	US-10-756-149-4702	Sequence 14, Appl
30	1370.5	66.9	390	5	US-10-723-955-14	Sequence 8, Appli
31	1370.5	66.9	390	5	US-10-488-421-8	Sequence 27, Appli
32	1366.5	66.7	390	4	US-10-290-078-27	Sequence 6, Appli
33	1366.5	66.7	390	5	US-10-488-421-6	Sequence 10, Appli
34	1237	60.4	389	5	US-10-626-445-10	Sequence 10, Appli
35	1237	60.4	389	5	US-10-626-126-10	Sequence 10, Appli
36	1237	60.4	389	5	US-10-626-398-10	Sequence 10, Appli
37	1198	58.5	357	5	US-10-488-421-4	Sequence 10, Appli
38	1074.5	52.5	336	5	US-10-488-421-2	Sequence 2, Appli
39	729.5	35.6	415	5	US-10-495-679A-8	Sequence 8, Appli
40	722.5	35.3	445	3	US-09-350-206-2	Sequence 2, Appli
41	722.5	35.3	445	3	US-09-349-755-2	Sequence 2, Appli
42	722.5	35.3	445	3	US-09-166-334-2	Sequence 2, Appli
43	722.5	35.3	445	4	US-10-282-958-2	Sequence 2, Appli
44	722.5	35.3	445	4	US-10-225-567A-549	Sequence 549, App
45	722.5	35.3	445	4	US-10-453-106-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-626-445-8
; Sequence 8, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-445-8

Query Match 100.0%; Score 2048; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 6.8e-180;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSESNTGILPPAAQVPLAFILMSFAFAIMVGNNAVILAFVVDRLNLRHRSNYFFLNLAIS	60
Db	1	MSESNTGILPPAAQVPLAFILMSFAFAIMVGNNAVILAFVVDRLNLRHRSNYFFLNLAIS	60
Qy	61	DFLVGLISILYIPLVFLNFGSGICMFWLITDYLLCTASVNVILISYDRYOSVNAV	120
Db	61	DFLVGLISILYIPLVFLNFGSGICMFWLITDYLLCTASVNVILISYDRYOSVNAV	120
Qy	121	SYRAQHTGIMKIIVAQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYLLIT	180
Db	121	SYRAQHTGIMKIIVAQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYLLIT	180
Qy	181	MLLEFLPVTSVAYFNVQIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN	240
Db	181	MLLEFLPVTSVAYFNVQIYVSLWKRRALSRCPSHAGFTSTSSASGHLHRAGVACRTSN	240
Qy	241	PGLKESAAHSHSPRKSILVSLRTHMNSSITAFKVGFWRSSEALRQREYAEILRG	300
Db	241	PGLKESAAHSHSPRKSILVSLRTHMNSSITAFKVGFWRSSEALRQREYAEILRG	300
Qy	301	RKLARSAILLSAFAICWAPYCLFTIIVLSTVPRTERPKSVWYSTAFWLOWNSFNPNPLY	360
Db	301	RKLARSAILLSAFAICWAPYCLFTIIVLSTVPRTERPKSVWYSTAFWLOWNSFNPNPLY	360

QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 2

US-10-626-126-8
; Sequence 8, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-126-8

Query Match 100.0%; Score 2048; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 6.8e-180;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDRLRHRNSYFFLNLAIS 60
Db 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDRLRHRNSYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLIITDYLLCTASVNVILISYDRYQSVNAV 120
Db 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLIITDYLLCTASVNVILISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFTWYILITIT 180
Db 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFTWYILITIT 180
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
QY 241 PGLKESAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300
Db 241 PGLKESAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
Db 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 3

US-10-626-398-8
; Sequence 8, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-398-8

Query Match 100.0%; Score 2048; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 6.8e-180;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDRLRHRNSYFFLNLAIS 60
Db 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDRLRHRNSYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLIITDYLLCTASVNVILISYDRYQSVNAV 120
Db 61 DFLVGLISIPLYIPIHVLFNWFGSGICMFWLIITDYLLCTASVNVILISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFTWYILITIT 180
Db 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFTWYILITIT 180
QY 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
Db 181 MLLEFLLPVISVAYFNVQIYWSLWKRRLSRCPSHAGFTSTSSASGHLHRAGVACRTSN 240
QY 241 PGLKESAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300
Db 241 PGLKESAASHSPRRKSSILVSLRTHMNSSITAFKVGFWKSESAAALQREYAEALLRG 300
QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
Db 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
QY 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391

RESULT 4

US-10-626-445-9
; Sequence 9, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-445-9

Query Match 84.7%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 4.7e-151;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDRLRHRNSYFFLNLAIS 60

Db 1 MSESNGTDVLPPLTAQVPLAFVLSLAFATIGNAVVILAFVADRNLHRNSYFFLNLAIS 60
Qy 61 DFLVGLISIPLYIPHTLFFNNPFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFFNNPFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
Qy 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180
Db 121 RYRAQHTGILKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPHAGFSTTSSASGHLHRAGVACRTSN 240
Db 181 AFLEFLLPVLSLVYFVSQIYWSLWKRRALSRCPHAGFIATSSRGTHSRRGTGLACRTSL 240
Qy 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSITAFKVGFWRSSESAALRQREYAEILLRG 300
Db 241 PGLKEPAASLHSESPRCKSSLLVSLRTHMNSIIAFKVGFCRSESPVLHQREHVELLRG 300
Qy 301 RKLARSAILLSAFAPICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNFSVNPPLY 360
Db 301 RKLARSILAVLSAFAPICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNFSINPPLY 360
Qy 361 PLCHRRFQKAFWKILCVTKWPAISONOSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 5

US-10-626-126-9
; Sequence 9, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-126-9

Query Match 84.7%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 4.7e-151;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;
Qy 1 MSESNGTDVLPPLTAQVPLAFVLSLAFATIGNAVVILAFVADRNLHRNSYFFLNLAIS 60
Db 1 MSESNGTDVLPPLTAQVPLAFVLSLAFATIGNAVVILAFVADRNLHRNSYFFLNLAIS 60
Qy 61 DFLVGLISIPLYIPHTLFFNNPFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFFNNPFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
Qy 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180
Db 121 RYRAQHTGILKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPHAGFSTTSSASGHLHRAGVACRTSN 240
Db 181 AFLEFLLPVLSLVYFVSQIYWSLWKRRALSRCPHAGFIATSSRGTHSRRGTGLACRTSL 240
Qy 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSITAFKVGFWRSSESAALRQREYAEILLRG 300
Db 241 PGLKEPAASLHSESPRCKSSILVSLRTHMNSIIAFKVGFCRSESPVLHQREHVELLRG 300

Db 241 PGLKEPAASLHSESPRCKSSILVSLRTHMNSIIAFKVGFCRSESPVLHQREHVELLRG 300
Qy 301 RKLARSAILLSAFAPICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNFSVNPPLY 360
Db 301 RKLARSILAVLSAFAPICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNFSINPPLY 360
Qy 361 PLCHRRFQKAFWKILCVTKWPAISONOSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 6

US-10-626-398-9
; Sequence 9, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-398-9

Query Match 84.7%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 4.7e-151;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;
Qy 1 MSESNGTDVLPPLTAQVPLAFVLSLAFATIGNAVVILAFVADRNLHRNSYFFLNLAIS 60
Db 1 MSESNGTDVLPPLTAQVPLAFVLSLAFATIGNAVVILAFVADRNLHRNSYFFLNLAIS 60
Qy 61 DFLVGLISIPLYIPHTLFFNNPFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFFNNPFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
Qy 121 SYRAQHTGIMKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180
Db 121 RYRAQHTGILKIIVAOQVAVVILAFVNGPMLASDSWKNSTNTKDCPFGFVTEWYILIT 180
Qy 181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPHAGFSTTSSASGHLHRAGVACRTSN 240
Db 181 AFLEFLLPVLSLVYFVSQIYWSLWKRRALSRCPHAGFIATSSRGTHSRRGTGLACRTSL 240
Qy 241 PGLKESAAHSRSPRRKSSILVSLRTHMNSITAFKVGFWRSSESAALRQREYAEILLRG 300
Db 241 PGLKEPAASLHSESPRCKSSILVSLRTHMNSIIAFKVGFCRSESPVLHQREHVELLRG 300
Qy 301 RKLARSAILLSAFAPICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNFSVNPPLY 360
Db 301 RKLARSILAVLSAFAPICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNFSINPPLY 360
Qy 361 PLCHRRFQKAFWKILCVTKWPAISONOSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 7

US-09-812-216-2
; Sequence 2, Application US/09812216
; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu

```
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match      66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY      1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db      1 MPTDNTINLSLSTRVTLAFMSSVAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
QY      61 DFLVGLISPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
Db      61 DFFVGVISIPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
QY      121 SYRAQHTGIMKIIVAOVAVVAVVILAFVNGPMLASDSKNSNTKDCBPGFVTEWYILIT 180
Db      121 SYRTQHTGVILKIVTLVAVVAVVILAFVNGPMLVSESKWDEGS--ECEPGGFSEWYILAIT 178
QY      181 MLEFLLPVISVAYFNVOIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
Db      179 SFLEFVIPVILVAYFNWNIYWSLWKRDHLSCQSHPLGTAVSSNICHSFGRLSRRSL 238
QY      241 PGLKESAASHSPSRKSSILVSLRTHMNSSITAFKVGFWSESAAALQREYAEALLRG 300
Db      239 SASTEVPASPSPSRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY      301 RKLARSLAILLSAFATCWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
Db      299 RRLAKSLAILLGVFVAVCWAPYSFLTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPFY 358
QY      361 PLCHRRFQKAFWKILCVTKWPAALSQ-NQSVSS 391
Db      359 PLCHKRFQKAFWKILCVTKWPAALSQ-NQSVSS 390

RESULT 8
US-09-910-411-2
; Sequence 2, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-910-411-2

Query Match      66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY      1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
Db      1 MPTDNTINLSLSTRVTLAFMSSVAFAMVGNVILAFVVDNRNLRHRSNYFFLNLAIS 60
QY      61 DFLVGLISPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
Db      61 DFFVGVISIPLYIPIHVLFNWFGSGICMFWLITDYLLCTASVNIIVLISVDRYQSVNAV 120
QY      121 SYRAQHTGIMKIIVAOVAVVAVVILAFVNGPMLASDSKNSNTKDCBPGFVTEWYILIT 180
Db      121 SYRTQHTGVILKIVTLVAVVAVVILAFVNGPMLVSESKWDEGS--ECEPGGFSEWYILAIT 178
QY      181 MLEFLLPVISVAYFNVOIYWSLWKRRALSRCPSHAGFSTSSASGHLHRAGVACTSN 240
Db      179 SFLEFVIPVILVAYFNWNIYWSLWKRDHLSCQSHPLGTAVSSNICHSFGRLSRRSL 238
QY      241 PGLKESAASHSPSRKSSILVSLRTHMNSSITAFKVGFWSESAAALQREYAEALLRG 300
Db      239 SASTEVPASPSPSRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY      301 RKLARSLAILLSAFATCWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFY 360
Db      299 RRLAKSLAILLGVFVAVCWAPYSFLTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPFY 358
QY      361 PLCHRRFQKAFWKILCVTKWPAALSQ-NQSVSS 391
Db      359 PLCHKRFQKAFWKILCVTKWPAALSQ-NQSVSS 390

RESULT 9
US-09-875-076-14
; Sequence 14, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liao, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-875-076-14

Query Match 66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNSGILPPAAQVPLAFIMGSFAIMGNAAVILAFVVDNLRHRSNYFFLNLAIS 60
DB 1 MPDNTNSTINLSLSTRTVLTAFFMSLVAFIMLGNALVILAFVVDNLRHRSNYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGGICWFWLITDYLCTASVNVILISYDRYQSVSNV 120
DB 61 DFFVGVISIPLYIPHLTFFWDGKEICVFWLITDYLCTASVNVILISYDRYQSVSNV 120
QY 121 SYRAQHTGIMKIVAMVAVILAFVNGPMILASDSWKNSTNTKDCBPGFVTEWYILIT 180
DB 121 SYRQHTGVKIVTLMVAVVILAFVNGPMILVSESWKDEGS--ECBPGFVTEWYILIT 178
QY 181 MLLEFLPLVLSVAVFVQVYVWLSLWKRALSRCPSHAGFTSTSSASGHLHRAGVACTSN 240
DB 179 SPLEFVIPVLVAVFVNNVYVWLSLWKRALSRCPSHAGFTSTSSASGHLHRAGVACTSN 238
QY 241 PGLKESAAHSHSPRKSSTILVSLRTHMNSSITAFKVGFSWRSESAAALRQREYAEALLRG 300
DB 239 SASTEVPAFHSERQQRKSLMFSRRTWMSNTTASKMGFSQSDSVALLHQREHVELLRA 298
QY 301 RKLARSLAILLSAFAICWAPCYLFTIVLSTYPRTERPKSVWYISAFWLFQNFNSVFNPLY 360
DB 299 RRLAKSLAILLGVAVCWAPCYLFTIVLSTYPRTERPKSVWYISAFWLFQNFNSVFNPLY 358
QY 361 PLCHRRFOKAFKILCVTKWKPALSO--NQSVSS 391
DB 359 PLCHKRFQKAFKIFCIKKQPLPSQHSRVSS 390

RESULT 10
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-05-28
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; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
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; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match          66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDRLNHRNSYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKLNHRSSYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHTLFENDFGKEICVFWLITDYLCTASVNVILISYDRYLSVNAV 120
QY 121 SYRAQHTGIMKIQAQVAVVILAFVNGPMLASDSWKNSTNTKDCPPGFVTEWYILIT 180
DB 121 SYRTQHTGVLIKIVTLMAVAVVILAFVNGPMLVSESWKDEGS--ECEPGFSEWYILAIT 178
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIPVLVAYFNNIYWSLWKRDHLSCQSHPGCLTAVSSNICGHSFGRLLSSRRSL 238
QY 241 PGLKESAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALQREYAEILRG 300
DB 239 SASTEVPASPHSERQRRKSSLMFSSRTKMNSNTIASKMGFSQSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAIIILSAFAICWAPYCLFTIVLSTYPTERPCKSVWYSIAFWLQWNSFVNPLY 360
DB 299 RRLAKSLAIIILGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358
QY 361 PLCHRRFQKAFMKILCVTKWPALSO-NQSVSS 391
DB 359 PLCHKRFQKAFKLFCIKKQPLFSQHSRSVSS 390

RESULT 12
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1el Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match          66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFIMVGNVILAFVVDRLNHRNSYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKLNHRSSYFFLNLAIS 60
QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHTLFENDFGKEICVFWLITDYLCTASVNVILISYDRYLSVNAV 120
QY 121 SYRAQHTGIMKIQAQVAVVILAFVNGPMLASDSWKNSTNTKDCPPGFVTEWYILIT 180
DB 121 SYRTQHTGVLIKIVTLMAVAVVILAFVNGPMLVSESWKDEGS--ECEPGFSEWYILAIT 178
QY 181 MLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACRTSN 240
DB 179 SFLEFVIPVLVAYFNNIYWSLWKRDHLSCQSHPGCLTAVSSNICGHSFGRLLSSRRSL 238
QY 241 PGLKESAASHSESPPRKSSILVSLRTHMNSSITAFKVGSPWRSSESAALQREYAEILRG 300
DB 239 SASTEVPASPHSERQRRKSSLMFSSRTKMNSNTIASKMGFSQSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAIIILSAFAICWAPYCLFTIVLSTYPTERPCKSVWYSIAFWLQWNSFVNPLY 360
DB 299 RRLAKSLAIIILGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYIAFWLQWNSFVNPLY 358

RESULT 11
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00231regus
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USSN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2

Query Match          66.9%; Score 1370.5; DB 3; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
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QY 61 DFLVGLISIPLYIPHLVFNWFGSGICMFWLITDYLCTASVNVILISYDRYQSVNAV 120
DB 61 DFFVGVISIPLYIPHTLFENDFGKEICVFWLITDYLCTASVNVILISYDRYLSVNAV 120
QY 121 SYRAQHTGIMKIQAQVAVVILAFVNGPMLASDSWKNSTNTKDCPPGFVTEWYILIT 180
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QY 361 PLCHRRFQKAFKILCVTKWPAISO-NQSVSS 391
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RESULT 13

US-10-052-193-2

; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2

Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

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Db 121 SYRTQHTGVKIVTLVAVVWVILAFVNGPMLVSESWKDEGS--ECBPFGFSEWYILAIT 178
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QY 361 PLCHRRFQKAFKILCVTKWPAISO-NQSVSS 391
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RESULT 14

US-10-225-567A-629

; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-629

Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

QY 1 MSESNTGILPPAAQVPLAFMSSFAFAMVGNVILAFVVDNLRHRSYFFLNLAIS 60
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Db 61 DFFVGVISIPLYIPIHVLFEWDFGKEICVFWLITDYLCTASVNVILISYDRYQSVNAV 120
QY 121 SYRAQHTGIMKIVAQVAVVWVILAFVNGPMLASDSWKNSNTKDCPFGFVTEWYILIT 180
Db 121 SYRTQHTGVKIVTLVAVVWVILAFVNGPMLVSESWKDEGS--ECBPFGFSEWYILAIT 178
QY 181 MLLEFLLPVLSVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSASGHLHRAGVACTSN 240
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QY 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYISIAFWLQWNSFVNPPFLY 360
Db 299 RRLAKSLAILLGVAVCWAPYSLFTIVLSFYSSATGPKSVWYIRIAFWLQWNSFVNPPFLY 358
QY 361 PLCHRRFQKAFKILCVTKWPAISO-NQSVSS 391
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RESULT 15

US-10-272-983-14

; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567

; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-272-983-14

Query Match 66.9%; Score 1370.5; DB 4; Length 390;
Best Local Similarity 68.1%; Pred. No. 1.8e-117;
Matches 267; Conservative 40; Mismatches 82; Indels 3; Gaps 2;

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Db      61 DFFVGVISIPLYIPHYLVFNWFGSGICMEFLIITDYLLCTASVYNIVLISYDRYLSVNAV 120

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Db      121 SYRTQHTGVLKIVTLMAVAVMILAFLVNGPMILVSESWKDEGS--ECEPGPFSEWYILAIT 178

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QY      301 RKLARSLAILLSAPACWAPCYCLFTIVLSTYPTERPCKSVWYSIAFWLQWNSFVNPFY 360
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QY      361 PLCHRRFQKAFWKILCVTKWPALSO-NQSVSS 391
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Job time : 86 secs

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OM protein - protein search, using sw model

Run on: May 24, 2006, 13:35:45 ; Search time 10 Seconds
(without alignments)
435.470 Million cell updates/sec

Title: US-10-626-445-8
Perfect score: 2048
Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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- Database : Published Applications AA New.*
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 - 2: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	295.5	14.4	357	7	US-11-302-678-38
3	295.5	14.4	359	6	US-10-511-937-2990
4	292.5	14.3	440	7	US-11-302-678-41
5	283	13.8	269	7	US-11-305-477-3
6	267	13.0	465	7	US-11-255-699-4
7	236.5	11.5	403	7	US-11-242-505A-18
8	214.5	10.5	364	7	US-11-255-699-1
9	206.5	10.1	362	7	US-11-312-958-24
10	206.5	10.1	366	7	US-11-255-699-2
11	206	10.1	423	7	US-11-312-958-12
12	204	10.0	380	6	US-11-302-678-20
13	203	9.9	368	6	US-10-511-937-2505
14	203	9.9	368	6	US-10-511-937-2931
15	203	9.9	368	7	US-11-302-678-59
16	200.5	9.8	384	7	US-11-304-129-36
17	200.5	9.8	384	7	US-11-312-958-6
18	199.5	9.7	378	6	US-10-511-937-2404
19	197.5	9.6	412	7	US-11-242-505A-15
20	196.5	9.6	381	7	US-11-304-129-49
21	196.5	9.6	393	7	US-11-304-129-1
22	196.5	9.6	393	7	US-11-312-958-8
23	195.5	9.5	389	7	US-11-302-678-35
24	192	9.4	421	7	US-11-304-129-47
25	189	9.2	360	7	US-11-257-851A-75

26	187	9.1	393	7	US-11-304-129-40	Sequence 40, Appl
27	187	9.1	393	7	US-11-304-129-48	Sequence 48, Appl
28	178.5	8.7	352	6	US-10-505-328-745	Sequence 745, App
29	178.5	8.7	352	6	US-10-511-937-2486	Sequence 2486, Ap
30	178.5	8.7	352	6	US-10-511-937-2935	Sequence 2935, Ap
31	178.5	8.7	352	6	US-10-511-937-3010	Sequence 3010, Ap
32	175	8.5	350	6	US-10-511-937-2609	Sequence 2609, Ap
33	173	8.4	352	6	US-10-511-937-2412	Sequence 2412, Ap
34	165.5	8.1	370	7	US-11-305-477-1	Sequence 1, Appl
35	164	8.0	297	7	US-11-257-851A-73	Sequence 73, Appl
36	159.5	7.8	360	7	US-11-242-111-19	Sequence 19, Appl
37	158	7.7	360	7	US-11-242-505A-3	Sequence 3, Appl
38	157.5	7.7	352	7	US-11-242-505A-6	Sequence 6, Appl
39	156.5	7.6	332	7	US-11-257-851A-77	Sequence 77, Appl
40	156	7.6	325	7	US-11-312-958-40	Sequence 40, Appl
41	156	7.6	325	7	US-11-257-851A-79	Sequence 79, Appl
42	155	7.6	373	7	US-11-312-958-10	Sequence 10, Appl
43	151	7.4	424	7	US-11-242-505A-33	Sequence 33, Appl
44	151	7.4	424	7	US-11-255-699-3	Sequence 3, Appl
45	137	6.7	351	6	US-10-511-937-2540	Sequence 2540, Ap

ALIGNMENTS

RESULT 1

US-11-242-505A-27

Sequence 27, Application US/11242505A

Publication No. US20060099656A1

GENERAL INFORMATION:

APPLICANT: Carroll, Joseph M.

APPLICANT: Healy, Aileen

TITLE OF INVENTION: Methods and Compositions for Treating

TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,

TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, c

FILE REFERENCE: WPI2001-288P1RCP10WNIM

CURRENT APPLICATION NUMBER: US/11/242,505A

CURRENT FILING DATE: 2005-10-03

PRIOR APPLICATION NUMBER: US 10/290,078

PRIOR FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: US 60/347,949

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: US 10/320,351

PRIOR FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: 60/341,606

PRIOR FILING DATE: 2001-12-17

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27

LENGTH: 390

TYPE: PRT

ORGANISM: Homo Sapiens

US-11-242-505A-27

Query Match 66.7%; Score 1366.5; DB 7; Length 390;
Best Local Similarity 67.9%; Pred. No. 4.2e-111;
Matches 266; Conservative 40; Mismatches 83; Indels 3; Gaps 2;

QY	1	MSESNTGILPPAAQVPLAFMSSFAFIMVGNVAVLAFVVDENLRHSNYFFLNLAIS	60
Db	1	MPDTNSTINLSLSTRVTLAFMGLVAFMGLMGLVAFVVDKLRHSYFFLNLAIS	60
QY	61	DFLVGLISILPIYIPHLFNNFSGICMFWLITDYLCTASVYVNIIVLISYDRYQSVSNV	120
Db	61	DFFGVVISILPIYIPHTLFEWDFGKEICVFWLITDYLCTASVYVNIIVLISYDRYLSVSNV	120
QY	121	SYRAQHTGIMKIYVAQVAVMILAFVNGPMILASDSWKNSTNTKDCBPGFVTEWILTIT	180
Db	121	SYRTQHTGVLKIVTLVMVAVLAFVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT	178
QY	181	MLIEFLLPVLSVAYFNVQIYWSLWKRLSRCSHAGFSTTSSASGHLHRAGVACRTSN	240
Db	179	SFLEFVPIVLVAYFNNMNIYWSLWKRLSRCSQHPGLTAVSSNICGHSFRGLSRRLS	238

Db 157 KLAS--AAAWVLSLMSLPLLVFADVQBGCTNASWPBPVGLWGAVFIITYTAVLGFAPL 214
Qy 189 -VISVAFNVQIYNSLWKRRALSRCPSHAGSTTTSSSASGHLHRAGVACRTSNFGLKESA 247
Db 215 LVICLCVLLIIV-----KVRA-----AGVRGC 237
Qy 248 ASRHSESPRRKSSILVSLRTHMSSITAFKVGSEFWRSSEALRQREYAEALLRGRKLARS 307
Db 238 VRRSE-----
Qy 308 AILLSAFAICWAPYCLFTIVLSTYPTERTPRKSV-WYSIAFWLQNFNSFVNPFLYPLCHRR 366
Db 251 LVVLVFPAGCWLPFTTNVNLVALPOEPASAGLFPFVILSVANSANCANPVLYGLSDN 310
Qy 367 FQKAFWKILCVTK 379
Db 311 PROSFQKVLCLRK 323

RESULT 9
US-11-312-958-24
; Sequence 24, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55034, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MPI02-027P1RNOVNM
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-312-958-24

Query Match 10.1%; Score 206.5; DB 7; Length 362;
Best Local Similarity 19.5%; Pred. No. 7.5e-11;
Matches 74; Conservative 71; Mismatches 129; Indels 105; Gaps 9;

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Db 36 PPWAPALSAVLIYTTAVDVVGNLVLVSLRNRKLRNAGNLFVLVSLALADLVVAFYPY 95

Qy 71 LYIPHLFNP-WNFGSGICMFWLITDYLLCTASVYVNIIVLSYDRYQSVSNAYS-----YRAQ 125
Db 96 LILVAIFYDQWALGEHCKKASAFVWGLSVGVSNITAIINRYCYICHSMAYHRIYRW 155
Qy 126 HTGIMKIVAQWAVMILAFVNGPMILASDKMKNSTNTKCEPGFVTEWYILTIT----- 180
Db 156 HTPL-----HICLIWLLTVALLBNFF-----VGSLEYDPRITSCTFIQTASTQYTA 202
Qy 181 --MLLEFLLPVISVAFNVQIYNSLWKRRALSRCPSHAGSTTTSSSASGHLHRAGVACRT 238
Db 203 AVVVIHEHLLPIAVVFCYLRITWLVLOAR-----AGVRGC 233
Qy 239 SNPKKESAAHSRSESPPRRKSSILVSLRTHMSSITAFKVGSEFWRSSEALRQREYAEALL 298
Db 234 AKP-----ESRLCLKPSDLRSFLTMF----- 254
Qy 299 RGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERTPRK--SVWYSIAFWLQNFNSFVN 356
Db 255 -----VVFVIFALCWAPLNCIGLAVAINQEMAPQIPEGLFVTSYLLAVFNSCLN 304
Qy 357 PFLYPLCHRRFQKAFWKIL 375
Db 305 AIVYGLLNQNFREYKRI 323

RESULT 10
US-11-255-699-2
; Sequence 2, Application US/11255699
; Publication No. US20060105393A1
; GENERAL INFORMATION:
; APPLICANT: APPEL, CHRISTIAN
; APPLICANT: ENDERLE, THILLO
; APPLICANT: ZOFFMANN, SANNAH JENSEN
; APPLICANT: PENSKI, MIREILLE
; TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS
; FILE REFERENCE: 22817
; CURRENT APPLICATION NUMBER: US/11/255,699
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: EP 04105285.3
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-255-699-2

Query Match 10.1%; Score 206.5; DB 7; Length 366;
Best Local Similarity 21.1%; Pred. No. 7.6e-11;
Matches 82; Conservative 74; Mismatches 112; Indels 121; Gaps 18;

Qy 17 PLAPLMSSFAFAMV-----GNAAVILAFVVDRLNRHSNYFFLNLAISDFLVGLISIP 71
Db 41 PLLAGVATATCVAFVVGIAGNLLTMLVVSFRRLRTTNLYLSSWAFSDLLI-FLCMLD 99
Qy 72 -----YIPHLFNVNFGSGIC-MFWLITDYLLCT-ASVYVNIIVLSYDRYQSVSNAYS 123
Db 100 LVRLWQYRP-----WNFGDLCKLPQVSE--SCTVATVLTITALSVERYFAICFPLRAK 152
Qy 124 AQHT-GIMKIVAQWAVMILAFVNGPM-ILASDSKKNST---NTKCEP-GFVTEWYIL 177
Db 153 VVVTGRVKLV--IFVIVAFCSAGIFVLVGVHEHGTDPWDTNECRPTFEFAVRSGLL 210
Qy 178 TITMLLE---FLLPVISVAFNVQIYNSLWKRRALSRCPSHAGSTTTSSSASGHLHRAGV 234
Db 211 TVWVWVSSIFFLPVFCLTVLYSLIGRLWRR----- 242
Qy 235 ACRTSNPGLKESAAHSRSESPPRRKSSILVSLRTHMSSITAFKVGSEFWRSSEALRQREY 294
Db 243 -----RRGDAVV-----GASLRDQNH 258
Qy 295 AELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPTERTPRKSVWYS-----IAF 346

[illegible]

GenCore version 5.1.8
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Run on: May 25, 2006, 13:51:33 ; Search time 7472 Seconds
(without alignments)
5019.428 Million cell updates/sec

Title: US-10-626-445-8

-Perfect score: 2048

Sequence: 1 MSESNTGILPPAAQVPLAF.....WKILCVTKPALSONQSVSS 391

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1745	85.2	1593	6 AF358860	AF358860 Rattus no
3	1682.5	82.2	1308	6 BC111862	BC111862 Mus muscu

C	4	1434.5	70.0	199837	6	AC131672	Mus muscu
	5	1372.5	67.0	1173	5	AY008280	Homo sapi
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	21	1370.5	66.9	1312	2	BD095598	Novel gua
	22	1370.5	66.9	1312	5	AB045370	Homo sapi
	23	1370.5	66.9	1316	5	BC069136	Homo sapi
	24	1370.5	66.9	1847	5	BC112348	Homo sapi
	25	1370.5	66.9	3689	2	AX549343	Sequence
	26	1366.5	66.7	3689	5	AF312230	Homo sapi
	27	1366.5	66.7	1227	2	BD097512	Novel gua
	28	1366.5	66.7	1265	5	AB044934	Homo sapi
	29	1357.5	66.3	1175	5	AB189711	Macaca fa
	30	1311.5	64.0	1291	14	AB053300	Sus scrof
	31	1238	60.4	1451	6	AF358858	Cavia por
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C	36	906	44.2	167296	12	AP002507	AC009668 Homo sapi
C	37	906	44.2	169144	5	AC090244	AC090244 Homo sapi
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ALIGNMENTS

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DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.
ACCESSION AF358859
VERSION AF358859.1 GI:15420534
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
AUTHORS Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation.
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
AUTHORS Direct Submission
TITLE Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
JOURNAL Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA

FEATURES
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1. .1538
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/mol_type="mRNA"

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/strain="BALB/c"
/db xref="taxon:10090"
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/codon_start=1
/product="histamine H4 receptor"
/protein_id="AAK97380.1"
/db xref="GI:15420535"
/translation="MSESNGTGLPPAAQVPLAFLMSSFAFLMVGNAVILAFVVDRL
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TNTKCEPGTFTYILITIMLLEFLIPISVAYFNQIYVSLMKRALRSLRCSHAGF
STTSASGHLHRAVACSTNPLKESAAHRSSESPRRKSSILVSLRTHMNSISIAF
KVGSPWRSSEALRQREYAEALLRKLARSLAILLSAFAICWAPYCLFTIVLSTYPT
ERYKSVWYSIAFWLQFNSFVNPFLPLCHRRFQKAFWKLLCVTKQPALSONQSVSS"
ORIGIN

Alignment Scores:
Pred. No.: 7,43e-202 Length: 1538
Score: 2035.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.4% Indels: 0
DB: 6 Gaps: 0

US-10-626-445-8 (1-391) x AF358859 (1-1538)

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DB 241 GACTTCTCTGCTGGTTTGAATTTCCATTCCTCTGTACATCCCTCACGTTGTTTAACTGG 300
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DB 301 AATTTTGGAAAGTGAATCTGATGTTTGGCTCATCTACTGACTATCTTTTGTGCACCGCA 360
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 361 TCTGTCTACAATATTGCTCTCATTTAGTACGATCGATACCATCAGTTCCTCAAAATGCTGTG 420
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
DB 421 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTTG 480
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
DB 481 ATACTGGCTTCTTGGTAAATGGCCCATGATTTCTGGCTTCAGATTCTTGGAAAGACAGC 540
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DB 541 ACGACACAAAGACTCTGAGCCTGGCTGTTTACAGAGTGGTATCATCTCCACCATTTACA 600
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DB 601 ATGCTCTTGGAAATTCCTGCTCTCTCATCTCTGCTGCTTATTTCAATGTACAGATTAC 660
QY 201 TrpSerLeuTyrLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 661 TGGAGCCTGTGGAGCGTAGGCTCTCTCAGTAGGTCCTAGCCTAGCCTAGCCTTCCACT 720
QY 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
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DB 721 ACCTCTCCAGTGCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 780
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QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
DB 841 ATCTCTGGTGCTTTAAGGACTCATCATGACAGCAGTATCACTGCCCTTCAAAGTGGGTTC 900
QY 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
DB 901 TTTCTGGCGATCGAAAGTTCGAGCGCTTCGCAAAAGGAGTACGACAGAGCTTCTCAGAGC 960
QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
DB 961 AGGAAGCTAGCAGGTCATCGGCCATCTCTGAGGCGCTTTTGGCATTTCTGGGCTCCA 1020
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
DB 1021 TACTGTCTGTTCACAATTTGCCCTTCAACTTATCCCCAGAAACGAGCCCAATCGGTG 1080
QY 341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
DB 1081 TGGTACAGCATTTGCTTCTGGCTGCAATGCTTCAATTCGTTTGTATCCCTTCTGTATC 1140
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380
DB 1141 CCTTTGTGTACAGGCTTTCAGAAAGCTTCTTGGAAAGTACTTTGTGTGACAAAGCAA 1200
QY 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
DB 1201 CCAGCGCTGTACACAAACAGTCAGTCACTATCTTCT 1233

RESULT 2
AF358860 1593 bp mRNA linear ROD 02-SEP-2001
LOCUS Rattus norvegicus histamine H4 receptor mRNA, complete cds.
DEFINITION AF358860
ACCESSION AF358860.1 GI:15420536
VERSION
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 1593)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation
Unpublished
2 (bases 1 to 1593)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
FEATURES
source
1. .1593
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
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/codon_start=1
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/protein_id="AAK97381.1"
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TNTKCEPGTFTYILITIMLLEFLIPISVAYFNQIYVSLMKRALRSLRCSHAGF
STTSASGHLHRAVACSTNPLKESAAHRSSESPRRKSSILVSLRTHMNSISIAF
KVGSPWRSSEALRQREYAEALLRKLARSLAILLSAFAICWAPYCLFTIVLSTYPT
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CDS
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IATSSRGTHSRRTGLACRTSLPGLKBPAAHLHSESPRGKSSLLVSLRTHMSGSIAP
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ERPKSIWYSIAFWLQWENSLNPLFLCHRRFQKAPWKILCVTKQAPAPQOTQSVSS"

ORIGIN

Alignment Scores:
Pred. No.: 1,5e-171 Length: 1593
Score: 1745.00 Matches: 332
Percent Similarity: 89.3% Conservative: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 6 Gaps: 0

US-10-626-445-8 (1-391) x AF358860 (1-1593)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 36 ATGTCGGAGTCTAACGGCACTGACGTCTTCCACCTGCTCAAGTCCCTCGCATTT 95
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 96 TTAATGTCCCTGCTGCTTTTGTCTATACGATAGCAATGCTGTGTCATTTTAGCCCTT 155
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 156 GTACGACACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 215
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 216 GACTTCTTCGTGGGTGCATCTCCATCTCTGTACATCCCTCACGCTGTTAACTGG 275
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Db 276 AATTTTGGAAAGTGAATCTGCATGTTTGGCTATTACTGACTATCTTTTGTGCACAGCA 335
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Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140
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Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
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Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 636 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTCAGTACCCAGCTGGATTTCATCGCT 695
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 696 ACCTCTTCCAGGGCACTGGACACTCACGCAACTGGGTGGCTTTAGCAACAAGTCTT 755
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 756 CTGTGATTAAGGAACACCGCGCATCCCTTCATTCAAGAAATCCACGAGGAAGAGCAGT 815
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 816 CTCCTGGTGTCTTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 875
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300

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Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
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Db 1176 CCAGCCTTTCACAGACCCAGTCAGTATCTTCT 1208
RESULT 3
LOCUS BC111862 1308 bp mRNA linear ROD 16-JAN-2006
DEFINITION Mus musculus histamine H4 receptor, mRNA (cDNA clone MGC:130500
IMAGE:40046148), complete cds.
ACCESSION BC111862
VERSION BC111862.1 GI:84993254
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1308)
AUTHORS Straube, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smaluk, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1308)

CONSRMT
TITLE Mammalian Gene Collection Program Team
JOURNAL Generation and initial analysis of more than 15,000 full-length
PUBMED human and mouse cDNA sequences
AUTHORS Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
CONSRMT 12477932
JOURNAL 2 (bases 1 to 1308)
AUTHORS NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2006) National Institutes of Health, Mammalian
REMARK Gene Collection (MGC), Bethesda, MD 20892-2590, USA
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.ncm@hri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, O.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Turgenev, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAM Plate: 15 Row: C Column: 19.

FEATURES

Location/Qualifiers

source

1. 1308

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="MGC:130500 IMAGE:40046148"

/tissue_type="PCR rescued clones"

/clone_lib="NIH MGC 285"

/notes="Vector: PCR-Blunt II-TOPO with reversed insert;

Clone identification sequence tag: GTGGTTA"

gene

1. 1308

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/notes="synonyms: H4, H4R, BG26, HH4R, AXOR35, GPRV53,

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/db_xref="MGI:2429635"

283..1071

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/product="Hrh4 protein"

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/db_xref="MGI:2429635"

/translation="MKIVQMVAWVILAFVNGPMLASDWSKNTNTKDCRGFTVE

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 ROREYAEILGRKLARSALLSAFAICWAPYCLFTIVLSTYPTERTPKSVWYSIAFW
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ORIGIN

Alignment Scores:

Pred. No.:	3.71e-165	Length:	1308
Score:	1682.50	Matches:	334
Percent Similarity:	85.2%	Conservative:	0
Best Local Similarity:	85.2%	Mismatches:	2
Query Match:	82.2%	Indels:	56
DB:	6	Gaps:	1

US-10-626-445-8 (1-391) x BC111862 (1-1308)

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Qy	21	LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe	40
Db	120	TTAATGCTTCATTTGGCTTTGCTATATATGTTAGGCAATGCTGGGTTCATCTTAGCCTTT	179
Qy	41	ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	180	GTGGTGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCT	239
Qy	61	AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr	80
Db	240	GACTTCCTC-----	248
Qy	81	AsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeuLeuCysThrAla	100

Db	248	-----	248
Qy	101	SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAla-Va	120
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Qy	120	lSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTr	140
Db	255	GTCTTATAGGCTCAACACACATGGCATCATGAAGATTGTTGCTCAAAATGGTGGCTGTTG	314
Qy	140	pIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSe	160
Db	315	GATACTGGCTTTCTTGGTAAATGCCGATGATTTCTGGCTTCAGATTCTTTGGGAAGAACAG	374
Qy	160	rThrAsnTyrLysAspCysGlyProGlyPheValThrGluTyrTrpIleLeuThrIleTh	180
Db	375	CACGAACACAAAGGACTGTGAGCTGGCTTTGTTCAGAGTGGTACATCTCCACATTAC	434
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Qy	240	nProGlyLeuLysGluSerAlaSerArgHisSerGluSerProArgArgLysSerSe	260
Db	615	TCTTGGATTGAAGGAATCAGTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	674
Qy	260	rIleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySe	280
Db	675	CATCTGGTGTCTTAAAGGACTCACATGAACAGCAGTATCAGTCCCTTCAAGAGTGGGTTTC	734
Qy	280	rPheTyrArgSerGlnSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGl	300
Db	735	CTTCTGGCGATCGGAAGTCCAGCGCTTCGCCAAAGGAGTACGACAGCTTCTCAGAGG	794
Qy	300	YArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPr	320
Db	795	CAGGAAGCTAGCCAGGTCCTCTGAGCGCTTTGCGCATTTTGGCTTTGCTGGGCTCC	854
Qy	320	oTyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVa	340
Db	855	ATACTGTCTTTCACAAATGCTCTTCACTTACCCAGAACGGAACGCCCAATCGGT	914
Qy	340	lTyrTyrSerIleAlaPheThrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTy	360
Db	915	GTGGTACAGCATTTGGCTTCTGGCTGCAATGTTCAATTCGTTTGTATTCCTTCTGTA	974
Qy	360	rProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTr	380
Db	975	CCCTTTGTGTACAGGCTTTCAGAGGCTTTCGGAAGATCTTGTGTGACAAAGCA	1034
Qy	380	pProAlaLeuSerGlnAsnGlnSerValSerSer	391
Db	1035	ACCAGCGCTGTACAGAACCAAGTACAGTATCTCTCT	1068

RESULT 4

AC131672/c

LOCUS

DEFINITION

AC131672

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC131672 199837 bp DNA linear ROD 11-FEB-2004
 Mus musculus chromosome UNK clone RP23-314021, complete sequence.

AC131672
 AC131672.3 GI:42517281

HTG.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
Wilson, R.K.

REFERENCE

1. (bases 1 to 199837)
The sequence of Mus musculus clone

REFERENCE

2. (bases 1 to 199837)
McPherson, J.D. and Waterston, R.H.
Direct Submission

REFERENCE

3. (bases 1 to 199837)
Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

REFERENCE

4. (bases 1 to 199837)
Submitted (06-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

REFERENCE

5. (bases 1 to 199837)
Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

COMMENT

On Feb 11, 2004 this sequence version replaced gi:38194370.

FEATURES

Location/Qualifiers
1. 199837
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-314021"

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu

Project Information

Center project name: M_BA0314021

ORIGIN

Alignment Scores:
Pred. No.: 6.82e-136 Length: 199837
Score: 1434.50 Matches: 296
Percent Similarity: 78.6% Conservative: 13
Best Local Similarity: 75.3% Mismatches: 33
Query Match: 70.0% Indels: 51
DB: 6 Gaps: 8

US-10-626-445-8 (1-391) x AC131672 (1-199837)

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Qy 24 SerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPheValAsp 43
Db 93399 GCTTTCTATTATAGATA-----GTGTCCATGCGCTTGCTACAGTGT 93358
Qy 44 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAppPheLeu 63
Db 93357 TCAAACTTT---CACCTGATGGTGATATTGTTGCTTGACAGTTATTGAGAAGCATGT 93301
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Db 93300 GCCACATCAGTCAGTAGTAGTCTTGTCATATCCC-----TGAAC 93256
Qy 82 PheGlySerGlyIleCysMetPheTrpLeu-----IleThrAspTyrLeuLeuCys 98
Db 93255 -----ARGTGTGTTTCAATAAACACATTAGTGTCTGCTGTTCTTG----- 93214
Qy 99 ThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn 118
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Qy 119 AlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAla 138
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Qy 139 ValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLys 158
Db 93153 GTTTGGATACGGCTTTCTTGGTAAATGGCCCGATGATTCCTGGCTTCAGATCTCTGGAG 93094
Qy 159 AsnSerThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThr 178
Db 93093 AACAGCAGCAACACAAAGGACTGTGAGCTGGCTTTGTTACAGAGTGTGTACATCCTCACC 93034
Qy 179 IleThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGln 198
Db 93033 ATTACAATGCTTTGGAAATTCCTGCTCTCATCTCTGCTGGCTTATTTCAATGTACAG 92974
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Qy 319 AlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLys 338
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Qy 339 SerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPhe 358
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Qy 359 LeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThr 378
Db 92493 CTGTACCTTTGTGTACAGCGCTTTCAGAGAGGCTTTCAGAGAGTACTTTGTGTGACA 92434
Qy 379 LysTrpProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 92433 AAGCAACACGCGCTGTACAGAACCCAGTCACTGATCTTCT 92395

RESULT 5
AY008280 1173 bp mRNA linear PRI 15-MAR-2004
LOCUS Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.
DEFINITION
ACCESSION AY008280
VERSION AY008280.1 GI:15822540
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1173)
AUTHORS Nguyen, T., Shapiro, D.A., George, S.R., Setola, V., Lee, D.K., Cheng, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and O'Dowd, B.F.


```

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ORIGIN
Alignment Scores:
Pred. No.: 1.19e-132 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2

US-10-626-445-8 (1-391) x AR142850 (1-1173)
Qy 1 MetSerGluSerAsnSerThrGlyIleuProAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAATACACAACTTATCAATGACATCTGCTGTACTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATGCTAGAAATGCTTTGGTCAATTTTAGCTTTT 120
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DEFINITION Novel polypeptide.
ACCESSION BD015847
VERSION BD015847.1 GI:22556984
KEYWORDS JP 2001211889-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Peter, B. and Olaylee, M.A.
TITLE Novel polypeptide
JOURNAL Patent: JP 2001211889-A 1 07-AUG-2001;
PFIZER INC
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PN JP 2001211889-A/1
PD 07-AUG-2001
PF 27-OCT-2000 JP 2000329359
PR 29-OCT-1999 GB 9925641.4, 20-APR-2000 GB 0009973.9 PI
BEAT PETER, MARK ANTONY OLAYLEE
PC C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04,
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PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/ PC
C12P21/02, C12Q1/02, G01N33/15, G01N33/50, G01N33/53//C12P21/08,
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Pred. No.: 1.19e-132 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2
US-10-626-445-8 (1-391) x BD015847 (1-1173)

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ACCESSION CS173186
VERSION CS173186.1 GI:77153219
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Chen, R.
TITLE Human Orphan G Protein-Coupled Receptors
JOURNAL Patent: EP 1580271-A 13 28-SEP-2005;
Arena Pharmaceuticals, Inc. (US)
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Pred. No.: 1370.50 Matches: 267
Score: 1370.50 Conservative: 40
Percent Similarity: 78.3% Mismatches: 82
Best Local Similarity: 68.1% Indels: 3
Query Match: 66.9% Gaps: 2
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LOCUS Sequence 13 from Patent EP1584683.
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ACCESSION CS178018
VERSION CS178018.1 GI:77733617
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1 Chen, R.
AUTHORS Human orphan g protein-coupled receptors
TITLE Patent: EP 1584683-A 13 12-OCT-2005;
JOURNAL Arena Pharmaceuticals, Inc. (US)
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ORIGIN

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Alignment Scores:
Pred. No.: 1.19e-132 Length: 1173
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Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2

US-10-626-445-8 (1-391) x CS178018 (1-1173)
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Score:              1370.50        Matches:    267
Percent Similarity: 78.3%          Conservative: 40
Best Local Similarity: 68.1%       Mismatches:  82
Query Match:        66.9%          Indels:     3
DB:                  2              Gaps:        2

US-10-626-445-8 (1-391) x AX109119 (1-1173)

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Qy      101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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Db      361 TCTTATAGAACTCAACATACTCGGGTCTTGAAGATTGTTACTCTGATGGTGGCGGTTGG 420
Qy      141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db      421 GTGCTGGCCCTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGA 480
Qy      161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db      481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGCCATCACA 534
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Qy      241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
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DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION  AX139113
VERSION     AX139113.1  GI:14274791
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS    Peter, B. and O'Reilly, M.A.
TITLE      G-protein coupled receptor-like polypeptide
JOURNAL    Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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Best Local Similarity: 68.1%       Mismatches:  82
Query Match:        66.9%          Indels:     3
DB:                  2              Gaps:        2

US-10-626-445-8 (1-391) x AX139113 (1-1173)

Qy      1 MetSerGluSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
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DEFINITION Sequence 1 from Patent WO0185786.
ACCESSION AX301763
VERSION AX301763.1 GI:17382844
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H.
TITLE Human histamine h 4? receptor
JOURNAL Patent: WO 0185786-A 1 15-NOV-2001;
American Home Products Corporation (US)
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Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 2 Gaps: 2
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GenCore version 5.1.8
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Title: US-10-626-445-8

Perfect score: 2048

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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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ID AAI70981 standard; CDNA; 1176 BP.

XX AAI70981;

XX 18-MAR-2002 (first entry)

XX Mouse histamine H4 receptor cDNA.

XX Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW diagnosis; gene therapy; ss.

OS Mus musculus.

XX WO200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WPI; 2002-114339/15.
 DR P-PSDB; AAM50565.
 XX
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
 PT the proteins, useful in gene therapy for treating diseases where it is
 PT beneficial to elevate mammalian histamine H4 receptor activity.
 XX
 XX Claim 4; Fig 5A; 92pp; English.
 PS
 XX The present sequence is that of a cDNA clone encoding a murine histamine
 CC receptor of the H4 subtype. The cDNA was isolated from a mouse spleen
 CC cDNA library. It shows 72.8% homology to the human H4 receptor coding
 CC region. The invention provides mammalian (human, mouse, rat and guinea
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
 CC recombinant host cells that produce active recombinant protein. The
 CC pharmacology of known histamine ligands is demonstrated. Mammalian
 CC histamine H4 receptor may be used in gene therapy for the treatment of
 CC diseases where it is beneficial to elevate mammalian histamine H4
 CC receptor activity. Recombinant protein is useful for identifying
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be
 CC useful for diagnosing, treating or preventing asthma, allergy,
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
 CC disorders of the neuroendocrine system, stress and spasticity
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 SQ Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

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 Score: 2035.00 Matches: 390
 Percent Similarity: 99.7% Conservative: 0
 Best Local Similarity: 99.7% Mismatches: 1
 Query Match: 99.4% Indels: 0
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US-10-626-445-8 (1-391) x AAI70981 (1-1176)

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 Db 61 TTAATGTCCTTCAATTTGCTTATATGATAGCAATGCTGGTCACTTAGCCCTT 120
 Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaLeuSer 60
 Db 121 GTGGTGACAGAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
 Qy 61 AspPheLeuValGlyLeuLeuSerIlePheProLeuTyrIleProHisValLeuPheAsnTyr 80
 Db 181 GACTTCCTCGTGGGTTTGGATTTCATTCCTCTGTACATCCCTCAGGTGTTTAACTGG 240
 Qy 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
 Db 241 AATTTTGGAGTGGAACTGCAATGTTTGGCTCATTTACTGATCTATCTTTGTGACCCGCA 300
 Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
 Db 301 TCTGCTCAATAATTTGCTCATTAGTACGATCAGTACCATCAGTTCAGATGCTGTG 360
 Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140
 Db 361 TCTTATAGGGTCAACACACTGGGATCATGAAGATTGTTGCTCAATTTGGTGGCTTTGG 420
 Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrTyrAsnSer 160
 Db 421 ATACTGGCTTCTTGGTAAATGGCCCGCATGATTTCTGGCTTCAGATTTTGGAGAACAGC 480
 Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180

Db 481 ACGAACACAAAGACCTGTGTAGCCTGGCTTTGTTTACAGAGTGGTACATCCTCCACCATTTACA 540
 Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
 Db 541 ATGCTCTTGGAAATCTCTGCTTCTGTCACTCTGTGGCTTATTTCAATGTACAGATTTAC 600
 Qy 201 TrpSerLeuTyrPlyArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
 Db 601 TGGAGCTGTGTGAAGCGTAGGGCTCTCAGTAGTGCCCTAGCCATGCTGATTTCTCCACT 660
 Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
 Db 661 ACCTCTTCCAGTCTTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720
 Qy 241 ProGlyLeuLysGluSerAlaLeuSerArgHisSerGluSerProArgArgLysSerSer 260
 Db 721 CTTGGATTTGAGGAATCAGCTGCTGATCTGTCACTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780
 Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
 Db 781 ATCTGTGTGCTTAAAGGACTCACATGAACAGCAGTATCATCTGCTTCAAAGTGGGTTC 840
 Qy 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuTyrGly 300
 Db 841 TTCTGGCGATTCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGAGAGCTTCTCAGAGGC 900
 Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
 Db 901 AGAAGCTAGCCAGGTCACGTGGCCATCTTCTGAGCGCTTTTGCCTTTCTGGCTCCA 960
 Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 961 TACTGTCTGTTCACAAATTTGCTTCACTTACCCAGAACGGAAACGCCCAATCGGTG 1020
 Qy 341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
 Db 1021 TGGTACAGCATTCGCTTCTGGCTGCAATGTTCAATTCGTTTGTAACTCTTCTGTATC 1080
 Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380
 Db 1081 CCTTTGTGTACAGCGCTTTCAGAGAGCTTTCTGGNAGATACTTTGTGTGACAAAGCAA 1140
 Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
 Db 1141 CCAGCGCTGTCCACAGAACCAAGTCAGTATCTTCT 1173

RESULT 2
 ADO30257
 ID ADO30257 standard; cDNA; 1538 BP.
 XX
 AC ADO30257;
 XX
 XX 29-JUL-2004 (first entry)
 XX
 DE Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
 KW cytosatic; antinflammatory; vasotropic; antidiagonal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 KW murine; gene; ss.
 XX
 OS Mus musculus.

XX WO2004040000-A2.
 XX 13-MAY-2004.
 XX 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 XX 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,
 XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
 XX WPI; 2004-390329/36.
 XX P-PSDB; ADO29497.
 XX
 XX Novel mammalian G protein coupled receptors, useful for identifying
 XX compounds that modulates diagnosing and treating disease condition
 XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
 XX pectoris, Parkinson's disease.
 XX
 XX Claim 151; SEQ ID NO 1360; 542pp; English.
 XX
 XX The invention relates to human and mouse G protein-coupled receptors
 XX (GPCRs) and nucleic acids encoding them. The invention also relates to
 XX sequences at least 90% identical to the GPCR proteins and nucleic acids
 XX of the invention; methods of treating, preventing or diagnosing diseases
 XX associated with GPCRs of the invention; methods of screening for
 XX compounds useful in the treatment of GPCR-related diseases; a transgenic
 XX mouse comprising a GPCR gene of the invention; a mouse comprising a
 XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 XX from the transgenic mice; kits comprising several mice, each of which has
 XX a mutation in a different GPCR gene of the invention; and kits comprising
 XX probes which hybridise to GPCR polynucleotides of the invention. The
 XX invention further discloses variants of the GPCR polypeptides and vectors
 XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 XX be used in the diagnosis, treatment or prevention of a wide variety of
 XX diseases including neurological disorders (e.g., Alzheimer's disease,
 XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 XX disorders of the adrenal gland; disorders of the colon or intestine
 XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 XX myocardial infarction); muscular disorders; blood disorders (e.g.,
 XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 XX diseases); and disorders of the kidney, liver, lung, breast, ovary,
 XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 XX thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
 XX nucleic acid of the invention. Note: The full sequence data for this
 XX patent did not form part of the printed specification; those sequences
 XX not shown were obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX SQ Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 3,07e-171 Length: 1538
 XX Score: 2035.00 Matches: 390
 XX Percent Similarity: 99.7% Conservative: 0
 XX Best Local Similarity: 99.7% Mismatches: 1
 XX Query Match: 99.4% Indels: 0
 XX DB: 12 Gaps: 0
 XX
 XX US-10-626-445-8 (1-391) x ADO30257 (1-1538)
 XX
 XX Qy 1 MetSerGluSerAsnSerThrGlyIleuProAlaAlaGlnValProLeuAlaPhe 20
 XX Db ATGTGGAGTCTAAAGTACTGGCATCTTGGCCACGACTGCTCAGGTCCTTGGCATTT 120

Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleuAlaPhe 40
 Db 121 TTAATGCTTTCATTTGGCTTTGCTATATATGTTAGCAATGCTGGTCACTCTTAGCCCTT 180
 Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
 Db 181 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATATTTTTTCTTAATTTGGCTATTCT 240
 Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
 Db 241 GACTTCTCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCAGCTGTGTTAACTGG 300
 Qy 81 AsnPheGlySerGlyIleCysMetPheTrpIleuThrAspTyrLeuLeuCysThrAla 100
 Db 301 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGACCCGA 360
 Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
 Db 361 TCTGCTACAAATATTTGCTTCATTTAGCTACGATCAGTACCATGTTTCAAATGCTGTG 420
 Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTrp 140
 Db 421 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGCTGCTGTTGG 480
 Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIysAsnSer 160
 Db 481 ATACTGGCTTTCTTGGTAAATGGCCCGATGATCTGGCTTCAGATTCTTGGAGAAGACG 540
 Qy 161 ThrAsnThrIysAspCysGlyProGlyPheValThrGluTyrIleLeuThrIleThr 180
 Db 541 ACGAACACAAAGGACTGTGAGCTGGCTTGTTCACAGTGGTACATCTCACCATTACA 600
 Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
 Db 601 ATGCTCTTGGAAATTCCTGCTCTCTGCTCATCTCTGCTGCTTATTTCATGTACAGATTAC 660
 Qy 201 TrpSerLeuTrpIysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
 Db 661 TGGAGCCTCTGGAAAGCGTAGGGCTCTCAGTAGGTGGCTTCCATGCTGGGATTTCTCCACT 720
 Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
 Db 721 ACCTTCTCCAGTGTCTCAGGACACTTACACAGACTGGGTGGCTTGCAGGACAAAGTAAT 780
 Qy 241 ProGlyLeuIysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
 Db 781 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTCGAAGAAGACGACG 840
 Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
 Db 841 ATCTGTGTGCTCTTAAGGACTCACATGAACAGCAGTATCATCTGCTTCAAAGTGGGTTCC 900
 Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
 Db 901 TTTTGGCGATCGGAAAGTGGAGGCTTCGCCAAAGGGAGTACGACAGAGCTTCTCAGAGGC 960
 Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
 Db 961 AGGAGTACGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCATTTGCTGGGCTCCA 1020
 Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 1021 TACTGTCTGTTCACAAATTTGCTTCACTTACCCCAAGACGGAACGCCCCCAATTCGGTG 1080
 Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
 Db 1081 TGGTACAGCATTCCTTCTGGCTGCAATGGTTCAAATTCGTTTGTATTCCTTCTGTGTAC 1140
 Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpIysIleLeuCysValThrLysTrp 380
 Db 1141 CCTTTGTGTACAGGCGTTTCCAGAGGCTTCTCTGGAAGATACCTTTGTGTGACAAAGCAA 1200
 Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391

```

Db      1201 CCAGCGCTGTGCACAGAACCGAGTCAAGTATCTCT 1233
RESULT 3
AAI70982
AC      AAI70982;
XX
XX      18-MAR-2002 (first entry)
XX
XX      Rat histamine H4 receptor cDNA.
XX
XX      Histamine H4 receptor; rat; antiasthmatic; antiallergenic;
KW      antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
KW      diagnosis; gene therapy; ss.
XX
XX      Rattus rattus.
XX
XX      W0200192485-A1.
XX
XX      06-DEC-2001.
XX
XX      22-FEB-2001; 2001WO-US005914.
XX
XX      31-MAY-2000; 2000US-0208260P.
XX
XX      (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
XX      Lovenberg T, Liu C;
XX
XX      WPI: 2002-114339/15.
XX      P-PSDB; AAM50566.
XX
XX      New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT      the proteins, useful in gene therapy for treating diseases where it is
PT      beneficial to elevate mammalian histamine H4 receptor activity.
XX
XX      Claim 4; Fig 5C; 92pp; English.
XX
XX      The present sequence is that of a cDNA clone encoding a rat histamine
CC      receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA
CC      library. It shows 72.5% homology to the human H4 receptor coding region.
CC      The invention provides mammalian (human, mouse, rat and guinea pig)
CC      histamine H4 receptor nucleic acid molecules (see AAI70980-83) and
CC      polypeptides (see AAM50564-67). The nucleic acids have been expressed in
CC      recombinant host cells that produce active recombinant protein. The
CC      pharmacology of known histamine ligands is demonstrated. Mammalian
CC      histamine H4 receptor may be used in gene therapy for the treatment of
CC      diseases where it is beneficial to elevate mammalian histamine H4
CC      receptor activity. Recombinant protein is useful for identifying
CC      modulators of the mammalian histamine H4 receptor. Such modulators may be
CC      useful for diagnosing, treating or preventing asthma, allergy,
CC      inflammation, cardiovascular and cerebrovascular disorders, non-insulin
CC      dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
CC      disorders of the neuroendocrine system, stress and spasticity
XX
XX      Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.:      1,47e-145      Length:      1176
Score:          1745.00      Matches:      332
Percent Similarity: 89.3%      Conservative: 17
Best Local Similarity: 84.9%      Mismatches: 42
Query Match:    85.2%      Indels:      0
DB:            6      Gaps:        0

US-10-626-445-8 (1-391) x AAI70982 (1-1176)
Qy      1 MetSerGluSerAsnSerThrGlyLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db      1 ATGTCCGAGTCTAAACGGCACTGACGCTCTTGCCACTGACTCTCAAGTCCCTCGGCAATT 60

21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
61 TTAATGTCCCTGCTGCTTTTGTATAGCAATGCTGTGTCATTTTAGCTTT 120
41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCT 180
61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
181 GACTTCTTCGTGGTGTCACTTCATTCCTCTGTACATCCCTCACACGCTGTTTAACGTG 240
81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
241 AATTTTGGAAAGTGAATTCGATGTTTGGCTCATTAAGTACTGACTATCTTTTGTGCACAGCA 300
101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
301 TCCGTCTACAGTATTTGCTCTATTAGCTACGATCGATACCCAGTCAGTTTCAAACGCTGTG 360
121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
361 CGTTATAGACACAGACACTGGCATCTCTGAAATTTGTTGCTCAATGGTGGCTGTTTG 420
141 IleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAAGCAGC 480
161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
481 ACCAACACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTTACA 540
181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
541 GCATTTCTTGAATTTCTCTGCTCCCTGCTCTCTCTGGTGGTCTATTTTCAGTGACAGATTTC 600
201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGGCTTAGCCACGCTGGATTTTCATCGCT 660
221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
661 ACCTCTTCCAGGGGCACTGGACACTCCGAGAACTGGGTGGCTTGTAGACAAAGTCTT 720
241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
721 CCTGGATTAAAGAAACAGCCGCTATCCCTTCATTTCAGAAAGTCCACGAGGAAAGAGCAGT 780
261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
781 CTCTGGTGTCTTAAAGGACTCACAATGAGCGGTAGTATCATCGCTTTCAAAGTGGGTTC 840
281 PheTrpArgSerGluSerAlaAlaLeuArgGluArgGluTyrAlaGluLeuLeuArgGly 300
841 TTCTGCGGATCAGAAAGCCCGAGTCTTCCACAGAGAGACGCTGGAGCTTCTCAGAGGC 900
301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
901 AGGAAGCTAGCCAGTCTGCTAGTCTGCTCTCTGAGTGTCTTTGCCATTTGCTGGGCTCCG 960
321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
961 TATTGCTGTTTCAATTTGTTCTTTTCACTTATCGCAGAGGGGAGCGCCCAATTCGATT 1020
341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
1021 TGGTACAGCATAGCTTTTGGCTACAGTGTTCATTTCAATTCATTTAATCCCTTTCTATAC 1080
361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
1081 CCTTTGTGCCACAGACGCTTTCAGAGGCTTCTTGAAGATACACTCTGTGTGACAAAGCAA 1140
381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391

```


QY 381 ProAlaLeuSerGln---AenGlnSerValSerSer 391
DB 1135 CCTTACCATCAACACACAGTCGGTCAGTATCTTCT 1170

RESULT 5
ID AAA46023 standard; cDNA; 1173 BP.
XX AAA46023;
XX 22-AUG-2000 (first entry)
XX Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical; mutant;
KW ss.
XX Homo sapiens.
OS
XX WO200022131-A2.
XX 20-APR-2000.
XX 13-OCT-1999; 99WO-US024065.
XX 13-OCT-1998; 98US-00170496.
XX 12-NOV-1998; 98US-0108029P.
XX 20-NOV-1998; 98US-0109213P.
XX 27-NOV-1998; 98US-0110060P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 18-MAR-1999; 99US-0123944P.
XX 12-MAR-1999; 99US-0123945P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123948P.
XX 12-MAR-1999; 99US-0123949P.
XX 12-MAR-1999; 99US-0123951P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 28-MAY-1999; 99US-0137567P.
XX 27-JUN-1999; 99US-0141448P.
XX 27-AUG-1999; 99US-0151114P.
XX 03-SEP-1999; 99US-0152524P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156633P.
XX 29-SEP-1999; 99US-0156634P.
XX 29-SEP-1999; 99US-0156653P.
XX 01-OCT-1999; 99US-0157280P.
XX 01-OCT-1999; 99US-0157281P.
XX 01-OCT-1999; 99US-0157282P.
XX 01-OCT-1999; 99US-0157293P.
XX 01-OCT-1999; 99US-0157294P.
XX 12-OCT-1999; 99US-00416760.
XX 12-OCT-1999; 99US-00417044.
XX (AREN-) ARENA PHARM INC.
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI; 2000-317986/27.
XX P-PSDB; AAB02831.
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
PT inverse or partial agonists useful as therapeutic agents.
XX Example 1; Page 88-89; 187pp; English.
XX

CC The present invention describes transmembrane receptors, preferably human
CC G protein coupled receptors (GPCR), for which the endogenous ligand is
CC unknown (orphan GPCR receptors). More specifically the present invention
CC relates to non-endogenous, constitutively activated versions of a human
CC GPCR. These non-endogenous human GPCRs can be useful for the direct
CC identification of candidate compounds as receptors agonists, inverse
CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,49e-112 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: Gaps: 2

US-10-626-445-8 (1-391) x AAA46023 (1-1173)
QY 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
DB 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
DB 61 TTTATGTCTTAGTACTTTTGTATTAATGCTAGGAAATGCTTTGGTCATTTAGCTTTT 120
QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCT 180
QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
DB 181 GACCTCTTTGTGGTGTGATCTCCATTCCTTTGTATACCTCCCTCACGCGTGTTCGAATGG 240
QY 81 AsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCAGTACTGACTATCTGTATTGTACAGCA 300
QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCTGTATATAACATTGTCTCATCAGCTATGATCGATACCTGTCACTCTCAAAATGCTGTG 360
QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
DB 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTACTCTGATGGTGGCGGTTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 GTGCTGGCTTCTTGTAGTAATGGGCCAATGATTCTAGTTCAGAGTCTTGGAGGATGAA 480
QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTrpIleLeuThrIleThr 180
DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
DB 535 TCATTTCTGGAAATTCGTGATCCCGAGTCATCTTAGTCGCTTATTTCACATGAATATTAT 594
QY 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
DB 595 TGGAGCTGTGGAGCGGTGATCATCTCAGTAGGTGCCAAAGCCATCTCGGAGTGCCT 654
QY 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
DB 655 GTCTCTTCCAAACATCTGTGGACACTATTTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisGluSerProArgArgLysSerSer 260
DB 715 TCTGCATCGACAGAAGTTCTCTGCATCTCTTTTCATTTCAGAGACAGAGAGAGATAGT 774

Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAAATGGGTTCC 834
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAGGGAACATGTGAACACTGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAGTCACTGCCATTCTCTAGGGGTTTGTCTGTTTGTGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTCTCTGTTCACAATTTGCTTCTTCAATTTATTTCTCAGCAACAGAGGCTCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTCCTTTTGCAATCTCTTTTGAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGGCTTCTTGAAAATATTTGTATATAAAGCAA 1134
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACACAGTCAGTCGGTCACTCTTCT 1170
RESULT 6
AAD01124
ID AAD01124 standard; cDNA; 1173 BP.
XX AC AAD01124;
XX DT 02-NOV-2000 (first entry)
XX DE Human orphan G protein-coupled receptor hRUP7 cDNA.
XX KW Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;
XX KW transmembrane receptor; signal cascade; ss.
XX OS Homo sapiens.
XX FH Key
XX FT 1. .1173
XX FT Location/Qualifiers
XX FT /*tag= a
XX FT /product= "hRUP7"
XX FT /note= "Human orphan G protein-coupled receptor"
XX PN WO200031258-A2.
XX PD 02-JUN-2000.
XX PF 13-OCT-1999; 99WO-US023687.
XX PR 20-NOV-1998; 98US-0109213P.
XX PR 16-FEB-1999; 99US-0120416P.
XX PR 26-FEB-1999; 99US-0121852P.
XX PR 12-MAR-1999; 99US-0123946P.
XX PR 12-MAR-1999; 99US-0123949P.
XX PR 28-MAY-1999; 99US-0136436P.
XX PR 28-MAY-1999; 99US-0136437P.
XX PR 28-MAY-1999; 99US-0136439P.
XX PR 28-MAY-1999; 99US-0136567P.
XX PR 28-MAY-1999; 99US-0137127P.
XX PR 28-MAY-1999; 99US-0137131P.
XX PR 29-JUN-1999; 99US-0141448P.
XX PR 29-SEP-1999; 99US-0156555P.
XX PR 29-SEP-1999; 99US-0156633P.
XX PR 29-SEP-1999; 99US-0156634P.
XX PR 29-SEP-1999; 99US-0156653P.
XX PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.
PR 01-OCT-1999; 99US-0157282P.
PR 01-OCT-1999; 99US-0157283P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
PR 12-OCT-1999; 99US-00417044.
XX (AREN-) ARENA PHARM INC.
XX PI Chen R, Dang HT, Liaw CW, Lin I;
XX DR WPI: 2000-400068/34.
XX DR P-PSDB; RAY71297.
XX PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for
XX PT use in the identification of G protein-coupled receptor agonists.
XX PS Claim 25; Page 59; 102pp; English.
XX CC The present sequence is a cDNA encoding hRUP7, an endogenous human orphan
XX CC G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned
XX CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
XX CC GPCR of the invention, like all GPCRs has seven transmembrane alpha
XX CC helices with an extracellular N-terminus and an intracellular C-terminus.
XX CC However, no endogenous ligands has yet been identified for the proteins
XX CC of the invention. The orphan GPCRs may be used in the identification of
XX CC their endogenous ligands, and to screen potential GPCR agonists and
XX CC antagonists for use as pharmaceutical agents. The proteins may also be
XX CC used in the study of GPCR-mediated signalling cascades, and to elucidate
XX CC their precise role in normal and diseased human conditions. Nucleic acid
XX CC encoding human orphan GPCRs may be used for tissue localisation in
XX CC expression analysis to provide information about their function in
XX CC healthy and pathological states
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.49e-112 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 3 Gaps: 2
US-10-626-445-8 (1-391) x AAD01124 (1-1173)
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGTACTAATAGCACAAATCAATTTATCAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGAAATGCTTTGGTCATTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAAGTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTCAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTGTCTCATCAGCTATGATCAGTACCTGTCTCAGTCTCAAAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATATCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420


```
Qy      81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db      241 GATTTTGAAGAAAGAAATCTGTATTTGGTCTCACTACTGACTATCTGTATGTACAGCA 300
Qy      101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db      301 TCTGTATATACATGTCCTCATCAGCTATGATCATACCTCTGAGTCTCAATGCTGTG 360
Qy      121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db      361 TCTTATAGAACTCAACATACTGGGTCTTGAAGATTGTTACTCTCATGCTGGTCCGTTTGG 420
Qy      141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db      421 GTGCTGGCCCTCTTAGTGAATGGGCCAATGATTCCTAGTTTCAGAGTCTTGAAGGATCAA 480
Qy      161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db      481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAAATGGTACATCTTCGCCATCACA 534
Qy      181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db      535 TCATCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAAATATTAT 594
Qy      201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db      595 TGGAGCCTGTGGAAGCGTGATCATCTAGTAGTGCCAAAGCCATCTCGGACTGCTGCT 654
Qy      221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db      655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGAGATCTCT 714
Qy      241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db      715 TCTGCATCGACAGAAGTTCCTGCATCCTTTTCATTTCAGAGACAGAGAGAGAGAGTAGT 774
Qy      261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db      775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATCAATTGCTTCCAAATGGGTTC 834
Qy      281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db      835 TTCTCCCAATCAGATCTGTAGCTCTTCCACCAAGGGAACATGTTGAACCTGTAGAGCC 894
Qy      301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db      895 AGGAGATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTTGCTGTTGCTGGCTCCA 954
Qy      321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db      955 TATTCTCTGTTCACAATGTCTTTCATTTTATTTATTCCTCAGCAACAGGTCCTTAATCAGTT 1014
Qy      341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnPropheLeuTyr 360
Db      1015 TGGTATAGAAATGCATTTGGCTTTCAGTGGTTCATTTCTTTGTCATCTCTTTTGTAT 1074
Qy      361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1075 CCATTGTGTACAGCGCTTCAAAAGCGCTTCTTGAANAATTTTGTATAAAGCAAA 1134
Qy      381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db      1135 CCTCTACCATCACACACAGTCGGTCTAGTATCTTCT 1170
```

RESULT 8

AAH24007

ID AAH24007 standard; cDNA; 1173 BP.

XX AC AAH24007;

XX DX 10-AUG-2001 (first entry)

XX

```
DE Human G protein-coupled receptor AXOR35 cDNA.
XX
KW AXOR35; human; G protein-coupled receptor; 7TM receptor;
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; bipolar disorder; depression; delirium; dementia;
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
KW macrophage; eosinophil; neutrophil; function modulation;
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
KW drug screening; signal transduction; transgenic animal; drug discovery;
KW 88.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1173
XX FT /*tag= a
XX FT /product= "Human AXOR35"
XX FT /note= "G protein-coupled receptor"
XX
XX WO200133221-A1.
XX 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029461.
XX
XX 02-NOV-1999; 99US-00431898.
XX 03-FEB-2000; 2000US-00497790.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X,
XX Michalovich D, Morrow DM, Zhu Y;
XX WPI; 2001-316464/33.
XX P-PSDB; AAB73622.
XX
XX Novel G-protein coupled receptor polypeptide and polynucleotide for
XX treating cancer, autoimmune, pulmonary, cardiovascular and neurological
XX disorders and for identifying modulators useful for treating asthma.
XX
XX Claim 2; Page 49-50; 54pp; English.
XX
XX The invention relates to the human G protein-coupled receptor AXOR35
XX (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
XX and variants, like all G protein-coupled receptors, AXOR35 has 7 putative
XX transmembrane domains and is involved in signal transduction. AXOR35 has
XX homology and structural similarity with G protein-coupled receptors such
XX as the human histamine H3 receptor. The invention also relates to
XX expression vectors and host cells comprising AXOR35 DNA, to recombinant
XX expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
XX and nucleotides may be used to treat a wide variety of disorders
XX including bacterial, fungal, protozoal and viral infections, particularly
XX HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
XX diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
XX urinary retention; acute heart failure; hypotension; hypertension; angina
XX pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
XX psychotic and neurological disorders such as anxiety, schizophrenia,
XX manic depression, depression, delirium, dementia, and severe mental
XX retardation, and dyskinesias, such as Parkinson's disease, Huntington's
XX disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
XX nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
XX antibodies may be used in screening compounds for their ability to
XX modulate AXOR35 activity or expression. Such AXOR35 modulators are
XX particularly useful for treating asthma, and inhibiting or promoting the
XX function of lymphocytes, macrophages, eosinophils or neutrophils in
XX asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
```

CC useful for diagnosing or determining susceptibility of an individual to a
 CC disease via the detection of abnormal levels of protein or mRNA, or via
 CC the detection of mutations in the corresponding gene. AXOR35 proteins are
 CC also useful for inducing an immunological response in a mammal against
 CC the above diseases, and for antibody production. AXOR35 nucleotides are
 CC also useful as diagnostic reagents, in chromosome localisation and tissue
 CC expression studies, and for producing transgenic animals useful in drug
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
 CC protein or fragments thereof, and are also useful for treating conditions
 CC associated with the expression of the AXOR35 protein. The present
 CC sequence represents cDNA encoding human AXOR35
 XX
 SQ

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,49e-112 Length: 1173
 Score: 1370.50 Matches: 267
 Percent Similarity: 78.3% Conservative: 40
 Best Local Similarity: 68.1% Mismatches: 82
 Query Match: 66.9% Indels: 3
 DB: 5 Gaps: 2

US-10-626-445-8 (1-391) x AAH24007 (1-1173)

QY 1 MetSerGluSerAenSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
 DB 1 ATGCCAGATACTAATAGCACAAATTTATCACTAAGCAGCTCGTGTACTTTAGCATTT 60
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAenAlaValIleLeuAlaPhe 40
 DB 61 TTTATGTCCTTAGTAGCTTTTGTCTAATGCTAGGAAATGCTTTGTCAATTTAGCTTTT 120
 QY 41 ValValAspArgAenLeuArgHisAenSerAsnTyrPhePheLeuAenLeuAlaIleSer 60
 DB 121 GTGGTGACAAACACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGGCCATCTCT 180
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
 DB 181 GACTTCTTTGTGGTGAGTCACTCCATTCCTTTGTACATCCCTCACAGCTGTTGCAATGG 240
 QY 81 AsnPheGlySerGlyIleCysMetPheThrIleuIleThrAspTyrLeuLeuCysThrAla 100
 DB 241 GATTTTGGAAAGGAATCTGTGATTTTGGTCTACTACTGACTATCTGTTATGTACAGCA 300
 QY 101 SerValTyrAenIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaVal 120
 DB 301 TCTGTATATAACATTTGCTCATCAGCTATGATCGATACCTGTGCTCAGTCTCAAAATGCTGTG 360
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 DB 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
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 DB 421 GTGCTGGCTCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAA 480
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 QY 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAenValGlnIleTyr 200
 DB 535 TCATCTTGGAAATTCGGTATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
 QY 201 TrpSerLeuTyrLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
 DB 595 TGGAGCCTGTGCAAGCGGTGATCATCTCAGTAGTGCCAAAGCCATCTCTGGACTGACTGCT 654
 QY 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAen 240
 DB 655 GTCTCTTCCCAACATCTGTGGGACATCTCATTTCAAGAGGTAGACTATCTTCAAGAGATCTCTT 714
 QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260

DB 715 TCTGCATCGACAGAGTCTCTGCATCTCTTCATTCAGAGAGACAGAGAGAGAGTAGT 774
 QY 261 IleLeuValSerLeuArgThrHisMetAenSerSerIleThrAlaPheLysValGlySer 280
 DB 775 CTATGTTTTCTTCAAGAACCAAGATGAATAGCAATACAAATTCCTTCCAAATGGGTTC 834
 QY 281 PheTyrArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
 DB 835 TTCTCCCATCAGATCTGTAGCTCTTCCACCAAGGGAACATGTTGAATCTGTAGAGCC 894
 QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
 DB 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTTGTGGGCTCCA 954
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 DB 955 TATTCTCTGTTCACAATTTGCCCTTTCATTTATTCCTCAGCAACAGCTCTTAATCATGTT 1014
 QY 341 TrpTyrSerIleAlaPheTyrLeuGlnTyrPheAenSerPheValAenProPheLeuTyr 360
 DB 1015 TGGTATAGATTGCAITTTTGCTTCAGTGTTCATTTCCATTCCTTGTCAATCTCTTTTGTAT 1074
 QY 361 ProLeuCysHisArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380
 DB 1075 CCATTGTGTACAGCGCTTTCAAAAGGCTTCTTGAATAATATTTTGTATATAAAAGCAA 1134
 QY 381 ProAlaLeuSerGln---AenGlnSerValSerSer 391
 DB 1135 CCTTACCATCAACACACAGCTCGTCTAGTATCTTCT 1170
 RESULT 9
 ABZ80663
 ID ABZ80663 standard; cDNA; 1173 BP.
 XX
 AC ABZ80663;
 DT 13-JUN-2003 (first entry)
 XX
 DE Human histamine receptor coding sequence.
 XX human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
 KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
 KW anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;
 KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
 KW psoriasis; receptor.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 CDS 1..1173
 FT /*tag= a
 FT /product= "Histamine receptor"
 XX
 PN US6204017-B1.
 XX
 PD 20-MAR-2001.
 XX
 XX 07-OCT-1999; 99US-00414010.
 XX
 XX 07-OCT-1999; 99US-00414010.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;
 PI Wang S;
 XX
 XX WPI; 2002-442063/47.
 DR P-PSDB; ABO98629.
 XX
 XX New nucleic acid encoding antigenic part of human histamine receptor,

XX (ORTH) ORTHO-MCNEIL PHARM INC.
 PA Lovenberg T, Liu C;
 XX WPI; 2002-114339/15.
 DR P-PSDB; AAM50564.
 XX
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding
 PT the proteins, useful in gene therapy for treating diseases where it is
 PT beneficial to elevate mammalian histamine H4 receptor activity.
 XX
 PS Claim 4; Fig 1; 92pp; English.
 XX
 CC The present sequence is that of cDNA clone pH4R encoding a human
 CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
 CC marrow cDNA library. The invention provides mammalian (human, mouse, rat
 CC and guinea pig) histamine H4 receptor nucleic acid molecules (see
 CC AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have
 CC been expressed in recombinant host cells that produce active recombinant
 CC protein. The pharmacology of known histamine ligands is demonstrated.
 CC Mammalian histamine H4 receptor may be used in gene therapy for the
 CC treatment of diseases where it is beneficial to elevate mammalian
 CC histamine H4 receptor activity. Recombinant protein is useful for
 CC identifying modulators of the human histamine H4 receptor. Such
 CC modulators may be useful for diagnosing, treating or preventing asthma,
 CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
 CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
 CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
 XX
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,49e-112 Length: 1173
 Score: 1370.50 Matches: 267
 Percent Similarity: 78.3% Conservative: 40
 Best Local Similarity: 68.1% Mismatches: 82
 Query Match: 66.9% Indels: 3
 DB: 6 Gaps: 2

US-10-626-445-8 (1-391) x AAI70980 (1-1173)

Qy 1 MetSerGluSerAnSerThrGlyLeuProAlaGlnValProLeuAlaPhe 20
 Db 1 ATGCCAGATACTAATAGCACAAATTTATCTACTAGACATCGTGTGTACTTTAGCATTT 60
 Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
 Db 61 TTTATGTCCTTAGTAGCTTTTGTATATGCTAGGAATGCTTGGTCATTTTAGCTTTT 120
 Qy 41 ValValAspArgAnLeuArgHisArgSerAsnTyrPhePheLeuAnLeuAlaIleSer 60
 Db 121 GTGGTGACAAACACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180
 Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
 Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTGCGAATGG 240
 Qy 81 AsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
 Db 241 GATTTTGGGAAGGAATCTGTGATTTTGGCTCACTACTACTACTATCTGTATGTATGTACAGCA 300
 Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
 Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATCATCCTGTCAGTCTCAAAATGCTGTG 360
 Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValIleValAlaGlnMetValAlaValTyr 140
 Db 361 TCTTATAGAACTCAACACTACTGGGGTCTTGAAGATTCTTCTCTGATGGTGGCGGTTTGG 420
 Qy 141 IleLeuAlaPheLeuValAnGlyProMetIleLeuAlaSerAspSerTyrPheAsnSer 160
 Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATTTCTAGTCTTTCAGAGTCTTGGAGGATGAA 480

Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
 Db 481 GGTAAGTGAACCTGGATTTTTCGGAATGGTATACATCTTGGCCATCACA 534
 Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAnValGlnIleTyr 200
 Db 535 TCATCTTGGAAATTCGTGATCCCACTCATCTAGTCGCTTATTTCAACATGAAATTTAT 594
 Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
 Db 595 TGGAGCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGGCCATCTGGAGTCACTGCT 654
 Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
 Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
 Qy 241 ProGlyLeuLysGluSerAlaIleSerArgHisSerGluSerProArgAlaGlySerSer 260
 Db 715 TCTGCATCGACAGAGTCTCTGCATCTTCAATTCAGAGACAGACAGAGGAGGAGAGTAGT 774
 Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerIleThrAlaPheLysValGlySer 280
 Db 775 CTCATGTTTCTCTCAAGAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGTTCC 834
 Qy 281 PheTrpArgSerGluSerAlaIleLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
 Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAATCTTGTAGAGCC 894
 Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaPro 320
 Db 895 AGGAGATAGCCCAAGTCACTGGCCATTTCTTAGGGGTTTTTGTGTTTGTCTGCTGCTTCA 954
 Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 955 TATTTCTGTTCACAAATTTGCTTTTCAATTTATTTCTCAGCAACAGGTCTTAAATCAGTT 1014
 Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAnSerPheValAnProPheLeuTyr 360
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 Qy 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
 Db 1075 CCATTTGTGCACAGCCCTTCAAAAGCTTCTTGAAATATATTTTGTATATAAAAGCAA 1134
 Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
 Db 1135 CCTTACCATCACACACAGTCGCTCAGTATCTTCT 1170

RESULT 12
 AAI67750
 ID AAI67750 standard; cDNA; 1173 BP.
 XX
 AC AAI67750;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Human histamine H4 receptor protein encoding cDNA.
 XX
 KW Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;
 KW antiasthmatic; antiallergic; neuroprotective; antidiabetic; human;
 KW cerebroprotective; cAMP modulator; gene therapy; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS l. 1173
 FT /*tag= a
 FT /product= "histamine H4 receptor"
 XX
 PN WO200185786-A2.
 XX
 PD 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US014527.
 XX 05-MAY-2000; 2000US-0202151P.
 PR 23-AUG-2000; 2000US-0227567P.
 PR 13-NOV-2000; 2000US-0247855P.
 XX (AMHP) AMERICAN HOME PROD CORP.
 XX Jones PG, Blatcher M, Wu S, Pausch MH;
 PI WPI; 2002-049442/06.
 DR P-PSDB; AAG66023.
 XX New histamine receptor, termed H4 useful for detecting H4 (antagonists
 PT for treating transplanted organ rejection, asthma, allergy, multiple
 PT sclerosis and rheumatoid arthritis.
 XX Claim 13; Fig 1; 66pp; English.
 XX The invention provides an isolated histamine receptor, H4, which binds
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
 CC receptor can be expressed by standard recombinant methodology. Cells
 CC expressing H4 receptor protein at a detectable level can suppress cyclic
 CC adenosine monophosphate (cAMP) formation when contacted with the H4
 CC receptor agonist. The H4 receptor and antibodies are used for identifying
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
 CC for treating transplanted organ rejection, asthma, allergies and
 CC autoimmune pathologies such as multiple sclerosis, type 1 diabetes,
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
 CC protein and nucleic acids are useful targets to identify drugs that are
 CC effective in treating disorders associated with histamine-regulated
 CC processes. Identification and isolation of H4 receptor provides for
 CC development of screening of molecules that interact with H4 receptors.
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease
 CC as described above. The H4 receptor polynucleotide is useful to treat or
 CC prevent a disorder associated with the function of H4 in peripheral blood
 CC leukocytes. The present sequence represents a cDNA encoding the human
 CC histamine H4 receptor protein
 XX
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,49e-112 Length: 1173
 Score: 1370.50 Matches: 267
 Percent Similarity: 78.3% Conservatives: 40
 Best Local Similarity: 68.1% Mismatches: 82
 Query Match: 66.9% Indels: 3
 DB: 6 Gaps: 2

US-10-626-445-8 (1-391) x AAI67750 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
 Db 1 ATGCCAGATACATAAGCACAATCAATTTATCACTAAGCAGCTCGTGTACTTTAGCATTT 60
 Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
 Db 61 TTTATGTCCTTAGTAGCTTTTGGCTATATGCTAGGAATGCTTTGGTCATTTTAGCTTTT 120
 Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
 Db 121 GTGGTGGNCAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCCATCTCT 180
 Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
 Db 181 GACTTCTTTGGGTGTGATCTCCATCTCTTTGTACATCCCTCACAGCTGCTTCCGAATGG 240
 Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
 Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTACTACTACTACTACTACTACTACT 300
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Db 301 TCTGTATATAACATTGCTCTCATCATGATGATCGATACCTGTCAGTCTCAAAATGCTGTA 360
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 Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
 Db 535 TCATTCCTGGAATTCGTGATCCCGATCCAGTCATCTTAGTCGTTATTTCAACATGAATATTAT 594
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 Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
 Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834
 Qy 281 PheTrpArgSerGluSerAlaLeuLeuArgGluArgGluTyrAlaGluLeuLeuArgGly 300
 Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGCTCAGAGCC 894
 Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTyrAlaPro 320
 Db 895 AGGAGATTGCCAAGTCACCTGGCCATCTCTTAGGGGTTTTTGTCTGTTGCTGGGCTCCA 954
 Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 955 TATTCCTGTTCACAAATGTCCTTTCATTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
 Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
 Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCAATTCCTTGTCAATCTCTTTTGTAT 1074
 Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTyr 380
 Db 1075 CCATTGTGTCACAGCGCTTTCAAAAGCCTTTCTGAAATATTTTGTATATAAAAGCAA 1134
 Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
 Db 1135 CCTCTACCATCACACACAGTCGTCGTCAGTATCTTCT 1170

RESULT 13
 ACA93262
 ID ACA93262 standard; cDNA; 1173 BP.
 XX ACA93262;
 XX 16-JUL-2003 (first entry)
 DT XX
 DE Human cDNA encoding GPCR hRUP7.
 XX Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;
 KW hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hPR1; hG2A;
 KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUF4; signalling cascade.
 XX

Db 1135 CCTTACCATCACACACAGTCGGTCAGTATCTTCT 1170
||||| :||||| :||||| :||||| :|||||

RESULT 14

ADG98759
ID ADG98759 standard; cDNA; 1173 BP.

XX AC ADG98759;
XX DT 11-MAR-2004 (first entry)
XX DE Human orphan GPCR cDNA, RUP7.
XX KW Human; G protein-coupled receptor; GPCR; research tool; gene; ss.
XX OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 1..1173
XX FT /*tag= a
XX FT /product= "Human GPCR protein"

XX US2003148450-A1.

XX 07-AUG-2003.

XX 17-OCT-2002; 2002US-00272983.

XX 20-NOV-1998; 98US-0109213P.

XX 16-FEB-1999; 99US-0120416P.

XX 26-FEB-1999; 99US-0121852P.

XX 12-MAR-1999; 99US-0123946P.

XX 12-MAR-1999; 99US-0123949P.

XX 28-MAY-1999; 99US-0136436P.

XX 28-MAY-1999; 99US-0136437P.

XX 28-MAY-1999; 99US-0136439P.

XX 28-MAY-1999; 99US-0136567P.

XX 28-MAY-1999; 99US-0137127P.

XX 28-MAY-1999; 99US-0137131P.

XX 29-JUN-1999; 99US-0141448P.

XX 28-SEP-1999; 99US-0156333P.

XX 29-SEP-1999; 99US-0156555P.

XX 29-SEP-1999; 99US-0156634P.

XX 12-OCT-1999; 99US-00417044.

XX (CHEN/) CHEN R.

XX (DANG/) DANG H T.

XX (LIAW/) LIAW C W.

XX (LINI/) LIN I.

XX Chen R, Dang HT, Liaw CW, Lin I;

XX WPI; 2003-897571/82.

XX P-PSDB; ADG98760.

XX New cDNA encoding a human G protein coupled receptor, useful for making a
XX probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR
XX identification of the expression of the receptor in tissue samples.

XX Claim 25; SEQ ID NO 13; 52pp; English.

XX The present invention provides novel human G protein-coupled receptor
XX (GPCR) proteins and their encoding nucleic acids. The invention is useful
XX for making a probe for dot-blot analysis and for RT-PCR identification of
XX the expression of the receptor in tissue samples. The invention is also
XX useful for identifying candidate compounds as inverse agonists, agonists
XX or partial agonists and as research tools in determining the location of
XX the receptors within the body. The present sequence is human orphan G
XX protein-coupled receptor cDNA.

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 3.49e-112 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 10 Gaps: 2

US-10-626-445-8 (1-391) x ADG98759 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATAGCACAAATTTATCTACTAGCACTCGTGTTACTTTAGCAATT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGCTATAATGCTAGGAATGCTTTGGTCATTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAnLeuAlaIleSer 60
Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACGCTGTTCGAATGG 240
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Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTTCAGAGGTAGACTATCTTCAAGAGAGATCTCT 714
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCTCTGCATCTCTTCATTTCAGAGACAGAGAGAGAGTAGT 774
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Db 775 CTCAATGTTTCTTCCAAAGACCAAGATGAATAGCAATACATATGTTCTCCAAATGGGTTC 834
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTTCACCAAGAGGAACATGTTGAATCTCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGTGGCTCCA 954

QY 321 TrrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
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 QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
 Db 1135 CCTTACCATCACAAACAGTCGGTCAGTATCTTCT 1170
 RESULT 15
 ABS57063
 ID ABS57063 standard; cDNA; 1173 BP.
 XX
 AC ABS57063;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Human cDNA encoding G-protein coupled receptor AXOR35.
 XX
 KW Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;
 KW macrophage; eosinophil; neutrophil; infection; transplant rejection;
 KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;
 KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;
 KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;
 KW psoriasis; urological disease; urinary retention; cardiovascular disease;
 KW myocardial infarction; hypotension; hypertension; pulmonary disorder;
 KW chronic obstructive pulmonary disease; cough; renal disease;
 KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;
 KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;
 KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
 KW graft versus host disease; osteoporosis.
 XX
 OS Homo sapiens.
 PH
 FT Key Location/Qualifiers
 CDS 1..1173
 FT /*tag= a
 FT /product= "AXOR35"
 XX
 PN US2002137054-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-JUL-2001; 2001US-00910411.
 XX
 PR 02-NOV-1999; 99US-00431898.
 PR 03-FEB-2000; 2000US-00497790.
 PR 20-OCT-2000; 2000US-00693761.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Aubart KM, Bergsma DJ, Fitzgerald L, Graybill TL, Li X;
 PI Michalovich D, Morrow DM, Zhu Y;
 XX
 DR WPI; 2003-074982/07.
 DR P-PSDB; ABG71960.
 XX
 PT Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for
 PT treating infections, gastrointestinal disorders, autoimmune disorders,
 PT urological diseases, cardiovascular diseases and cancer.
 XX
 PS Claim 2; Page 21-22; 24pp; English.
 XX
 CC The invention relates to an isolated G-protein coupled receptor
 CC polypeptide, AXOR35, (and its homologues and variants) and its encoding

CC polynucleotide (and its homologues, variants, complements and RNA
 CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35
 CC expression vector, producing a recombinant host cell by introducing the
 CC vector into a cell such that the host cell produces AXOR35, a membrane of
 CC the host cell expressing AXOR35, identifying/screening for agonists or
 CC antagonists of AXOR35 and inhibiting or promoting the function of
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,
 CC by administering to the patient AXOR35 agonists or antagonists. The
 CC agonist or antagonist identified is useful for treating a disease such as
 CC asthma, or for inhibiting or promoting the function of lymphocytes,
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an
 CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,
 CC for identifying compounds that are agonists or antagonists of AXOR35, as
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or
 CC viral infections), transplant rejection, gastrointestinal disorders (such
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,
 CC psoriasis), urological diseases (such as urinary retention),
 CC cardiovascular diseases (such as myocardial infarction), hypotension,
 CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary
 CC disease), cough, renal diseases (such as renal ischaemia),
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft
 CC versus host disease and osteoporosis. The present sequence is the cDNA
 CC encoding AXOR35
 XX
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3.49e-112 Length: 1173
 Score: 1370.50 Matches: 267
 Percent Similarity: 78.3% Conservative: 40
 Best Local Similarity: 68.1% Mismatches: 82
 Query Match: 66.9% Indels: 3
 DB: 10 Gaps: 2
 US-10-626-445-8 (1-391) x ABS57063 (1-1173)
 QY 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
 Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCTACTAGCACTCGTGTCTTACTTACGATTT 60
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValAlaIleLeuAlaPhe 40
 Db 61 TTTATGTCTCTAGTAGCTTTTGTCTATAATGCTAGAAATGCTTTGGTCATTTAGCTTTT 120
 QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
 Db 121 GTGGTGGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCT 180
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
 Db 181 GACTTCTTTGTGGGTGGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTCAATGG 240
 QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
 Db 241 GATTTTGGAAAGGAAATCTGTATTTTGGTCTCACTGACTATCTCTGTTATGTACGCA 300
 QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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 Db 421 GTGCTGGCTCTTCTAGTAGTAATGGCCAAATGATTCTAGTCTTTCAGAGTCTCTTGAAGATGAA 480
 QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180

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Db      481  GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAAATGGTACATCTCTTGCCATCACA 534
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Db      535  TCATTCTTGGAAATTCGTGATCCCGAGTCATCTTAGTCGCTTATTTCACACATGAATATTTAT 594
Qy      201  TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db      595  TGGAGCTGTGGAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGGACTGACTGCT 654
Qy      221  ThrSerSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db      655  GTCTCTTCCAACTCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy      241  ProGlyLeuLysGluSerAlaIaSerArgHisSerGluSerProArgArgLysSerSer 260
Db      715  TCTGCATCGACAGAAGTTCCTGCATCTCTTCATTTCAGAGACAGAGAGAGAGAGTAGT 774
Qy      261  IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db      775  CTCATGTTTTCCTCAGAAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGGTTC 834
Qy      281  PheTrpArgSerGluSerAlaIaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db      835  TTCTCCCAATCAGATCTCTGTAGCTCTTCACCAAGGGAACATGTTGAACCTGCTTAGAGCC 894
Qy      301  ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db      895  AGGAGATTAGCCCAAGTCACCTGGCCATTCTCTAGGGGTTTTTGTGCTGCTGGCTCCA 954
Qy      321  TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db      955  TATTCTCTGTTCACAATTGTCCTTTCATTTATTCTTCAGCAACAGGTCTCTAATCAGTT 1014
Qy      341  TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnPropheLeuTyr 360
Db      1015  TGGTATAGAAATTGCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTTGAT 1074
Qy      361  ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1075  CCATTGTGTCAACAGCGCTTTCAAAAGGCTTCTTGAAAAATATTTGTATATAAAAAAGCAA 1134
Qy      381  ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db      1135  CCTCTACCATCACAAACACACATCGGTGCTAGTATCTTCT 1170
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Job time : 1261 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)
5345.833 Million cell updates/sec

Title: US-10-626-445-8

- Perfect score: 2048

Sequence: 1 MSSNSTGILPPAAQVPLAF.....WKILCVTKWPALSONQSVSS 391

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Fgapop 6.0 , Fgapext 7.0
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Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb_est6:*
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7: gb_est2:*
8: gb_est7:*
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10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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7	453.5	22.1	558	9	DA308555	DA308555
8	432.5	21.1	791	10	DW582260	EST_ssal_
9	429.5	21.0	574	9	DA306992	DA306992
10	423	20.7	542	10	DW576242	EST_ssal
11	416	20.3	728	10	DT257276	JGI_CAAU8
12	415	20.3	672	4	CB556920	AMGNNUC:U
13	413	20.2	2633	6	CR859546	Pongo pyg
14	410	20.0	2967	6	AK138282	Mus muscu
15	410	20.0	3816	6	AK081248	Mus muscu
16	408.5	19.9	853	5	CD326085	AGENCOURT
17	405.5	19.8	3592	6	CR859367	CR859367
18	404.5	19.8	1773	14	AY400782	Pongo pyg
19	404	19.7	1770	14	AY400782	Homo sapi
20	404	19.7	3171	6	AK080950	Mus muscu
21	393	19.2	1946	6	AK156130	Mus muscu
22	392	19.1	1764	6	BC018330	Mus muscu
23	392	19.1	2503	6	AK139448	Mus muscu
24	392	19.1	2611	6	AK004891	Mus muscu
25	392	19.1	3050	6	AK043877	Mus muscu
26	389.5	19.0	1203	14	AY407499	Homo sapi
27	389.5	19.0	1440	14	AY404935	Pan trogl
28	388	18.9	2780	6	AK032763	Mus muscu
29	388	18.9	2831	6	AK047070	Mus muscu
30	388	18.9	2979	6	AK038480	Mus muscu
31	388	18.9	3783	6	AK046607	Mus muscu
32	385.5	18.8	1440	14	AY404934	Homo sapi
33	384.5	18.8	1203	14	AY407500	Pan trogl
34	380.5	18.6	1401	14	DQ029898	Homo sapi
35	374.5	18.3	1440	14	AY404936	Mus muscu
36	374	18.3	647	10	DV880423	LB02613.C
37	367.5	17.9	1072	14	AY398880	Homo sapi
38	367.5	17.9	2232	6	CR606112	full-leng
39	365	17.8	1200	14	AY407501	Mus muscu
40	363.5	17.7	1072	14	AY398881	Pan trogl
41	363	17.7	643	9	AL848045	AL848045
42	363	17.7	824	9	CX422842	CX422842
43	361.5	17.7	814	10	DT311294	JGI_X2663
44	360.5	17.6	1161	14	AY415607	DT311294
45	360.5	17.6	2578	6	AK045364	AY415607 Mus muscu

ALIGNMENTS

RESULT 1
BX643713
LOCUS
DEFINITION BX643713 839 bp mRNA linear EST 04-SEP-2003
DXFZP781C0629_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DXFZP781C0629_5", mRNA sequence.
ACCESSION BX643713
VERSION BX643713.1 GI:34478046
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 839)
AUTHORS Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Oeanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)
TITLE Unpublished (2003)
JOURNAL Contact: MIPS
COMMENT MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DXFZP781C0629) is available at the RZPD in Berlin.

Qy 43 AspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPhe 62
Db 125 GACAAACCTTACACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCTGACTTC 184
Qy 63 LeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyrAsnPhe 82
Db 185 TTTTGGGTGTGATCTCCATCTCTTTGTACATCCTCACACGCTGTTCGAATGGGATTTT 244
Qy 83 GlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 102
Db 245 GGAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCATCTGTA 304
Qy 103 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyr 122
Db 305 TATAACATTGTCCTCATCAGCTATGATGACATCTGTACAGTCTCAATGCTGTCTTAT 364
Qy 123 ArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyrIleLeu 142
Db 365 AGAAGTCAACATCTGGGCTCTGAAGATTGTTACTCTGTATGGTGGCGTTTGGGTGCTG 424
Qy 143 AlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsn 162
Db 425 GCCTTCTTAGTGAATGGCCCAATGATCTAGTTTTCAGAGTCTTGGAAAGGATGAAGGTAGT 484
Qy 163 ThrLysAspCysGluProGlyPheValThrCluTrpTyrIleLeuThrIleThrMetLeu 182
Db 485 -----GAATGTGAACCTGGATTTTTTTCGAATGGTACATCTCTGGCATCATCATTC 538
Qy 183 LeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSer 202
Db 539 TTGGAATTCGTATCCAGTCATCTTAGTTCGTTTATTTTCAACATGATATTTATTGGAGC 598
Qy 203 LeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrThrSer 222
Db 599 CTGTGGAAGCGTGATCATCTCAGTAGTGCACCAAGCCATCTCGACTGCTGCTCTCT 658
Qy 223 SerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArg 237
Db 659 TCCACATCTGT-GGACACTCATTTCAGAGGTAGACTATCTCTTCAGG 702
RESULT 3
AK140374
LOCUS AK140374 2625 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus adult male cortex cDNA, RIKEN full-length enriched library, clone:B530005H20 product:histamine receptor H 3, full insert sequence.
ACCESSION AK140374 1 GI:74150094
VERSION AK140374.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1
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Meth. Enzymol. 303, 19-44 (1999)
REFERENCE 2
10349636
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Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE 3
11042159
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Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Iehi,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,K., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadoya,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Pezole,G., Quackenbush,J., Schriml,L.M., Staebli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barah,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynchaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
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Nature 409 (6821), 685-690 (2001)
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Nature 420 (6915), 563-573 (2002)
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Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Gestin-Hemming, P., Gengeras, T.R., Gojobori, T., Green, R.E., Guerin, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huminicki, L., Iacono, M., Ikeo, K., Iwama, K., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keisio, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochin, I.V., Lareau, L.P., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuura, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J.F., Reid, J.F., Ring, B.Z., Ringwald, M., Roest, B., Ruan, Y., Salzberg, S.L., Sanderlin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hilde, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Wataniki, A., Okamura-Ono, Y., Suzuki, H., Kawai, J., and Hayashizaki, Y. FANTOM Consortium
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16141072

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RIKEN Genome Exploration Research Group
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Science 309 (5740), 1564-1566 (2005)
16141073

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Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wataniki, A., Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
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CONSTRM
TITLE
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PUBMED
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AUTHORS

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REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
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FEATURES
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YRAQDFTTRARRKMAVWVLAFLVLPALLSSEYLSGSSIEGHGCAEFFYNYFL
ITASTLEFTFPFLSVTFNLSIYLNIRLRLDGDREAGPPPPDPAQSSPPAPP
CMGCVKRGHGEAMPLRYGVGEAGPVETGAGLGGGGGGAASPTSSGSSRGP
RPSLRKRGKPSASLSLEKRMVQSITQIRLRLSRDKKVAKSLAIIVIFGLCWAP
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2602. .2607

polyA_signal

Alignment Scores:
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Score: 700.50 Matches: 162
Percent Similarity: 53.0% Conservative: 49
Best Local Similarity: 40.7% Mismatches: 128
Query Match: 34.2% Indels: 59
DB: 6 Gaps: 10

US-10-626-445-8 (1-391) x AK140374 (1-2625)

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Db 400 GCCAAAGTGTGGGCAACGCGTGGTATGCTCGCTTCGTGGCGGATTCGAGCTCCGC 459
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Db 520 TGCATCCCATTTGATGTATGACCTATGCTGACCGCGCTTGGACCTTTGGCGGCGCTC 579
Qy 87 CysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleVal 106
Db 580 TGCAAGCTGTGGTGGTGGTAGACTACCTACTGTGTGCTCCTCCTCAGTCTTCAACATCGT 639
Qy 107 LeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGlnHis 126
Db 640 CTGATCAGCTATGACCGATTCCTGTGCTAGTCACTCGAGCTGTCTCTACCGGGCCAGCAG 699
Qy 127 ThrGlyIleMetIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal 146
Db 700 GGGGACACAAAGACGGGCTGTGGGAAGATGGCACTGTGTGGTGTGGCTTCTCCTGCTG 759
Qy 147 AsnGlyProMetIleLeuAlaSerAspSerTrpIys-----AsnSerThr 161
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Db 871 ACCCTCGAGTCTTCCACACCTTCTCAGCGGTACCTTCTTCAACCTCAGCATCTACCTG 930
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Db 931 AACATCCAGAGCGGCGACTCGCTTCTCGCTGGATGGGGGGCCGAGAGGTGGTGCAGAACCC 990

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Qy 210 -----SerArgCysProSerHisAlaGlyPheSerThrThrSerSerSerAla 225
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Qy 226 SerGlyHis-----LeuHisArg-----AlaGlyValAla 235
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Qy 236 CysArgThrSerAsnProGlyLeu----- 243
Db 1111 GTTGAGACTGGGAGGCTCGGCTCGGGGTGCAGCGGTGAGCGGCTGCTCGCTCGCCT 1170
Qy 244 -----LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerIle 261
Db 1171 ACCTCCAGCTCCGGCAGCTCTCAAGGGGCACTGAGAGGCCACGC----- 1215
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Db 1216 -----TCACTCAAAGGGGCTCAAGCCATCAGCGTCTTCAGCGTCTTCGAGGAAGGC 1269
Qy 282 TrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArg 301
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Qy 302 LysLeuAlaArgSerLeuAlaLeuLeuSerAlaPheAlaIleCysTrpAlaProTyr 321
Db 1324 AAGGTAGCAAGTCGCTGCCTATCATCGTAGCATCTTTGGGCTCTGTGGGCCCGGTAC 1383
Qy 322 CysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerValTrp 341
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Db 1441 TACGAGAGCTCTTCTGGCTCTGTGGCCAACTCGGCGGTCAACCGCTCTTACCCA 1500
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RESULT 4
CF147822 732 bp mRNA linear EST 25-JUL-2003
LOCUS AGENCOURT_14740187 NIH_MGC_145 Homo sapiens cDNA clone
DEFINITION IMAGE:6971899 5', mRNA sequence.
ACCESSION CF147822
VERSION CF147822.1 GI:33244090
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 732)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapb-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB102 row: b column: 06
High quality sequence stop: 610.
Location/Qualifiers

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source
1. 732
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:6971899"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH_MGC_145"
/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores: 7.03e-38 Length: 732
Pred. No.: 482.50 Matches: 97
Score: 66.1% Conservative: 30
Percent Similarity: 50.5% Mismatches: 56
Best Local Similarity: 23.6% Indels: 9
Query Match: 5 Gaps: 3
DB:

US-10-626-445-8 (1-391) x CF147822 (1-732)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 125 CTGGCCGGCTTCATGGCGCTCATCGTGGCCAGCGTGTGGGCAAGCCGCTGTGTCATG 184
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 185 CTGCGCTTCGTGGCGGCTCGAGCTCCGACCCAGAACAACTTCTTCTCTCAACCTC 244
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 245 GCCATCTCCGACTTCTCTCGTGGCGCTCTGTGCATCCACACTGTATGTACCCCTACGTCGTG 304
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 305 ACAGCCGCTGGACCTTCGGCCGGGCTCTGCAAGCTGTGGCTGTAGTAGCAGTACCTG 364
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 365 CTGTGCACCTCTCTGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTCTGTGGTCTC 424
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 425 ACCGAGCGGTCTCATACCGGGCCAGCGGGTGCACACCGCGCGGCGAGTGCAGGAATG 484
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 485 CTGTGTGGTGGTGTGGCTTCTCTGTGTACGAGCAGCATCTCTG-----AGC 535
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 536 TGGAGTACCTGTCCGGGGGAGCTTCCATCCCGAGGGCCACTGCTATGCCAGTTCCTTC 595
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 596 TACAACCTGGTACTTCTTCATCAGCGCTTCCACACTGGAGTCTTTTACGCCCTCTCTCAGC 655
Qy 192 ValAlaTyrPheAsnValGlnIleTyrTrpSerLeu 203
Db 656 GTCACTTTCTTAACTTCACTCATCTACCTGAACATC 691

RESULT 5
CO959034 721 bp mRNA linear EST 17-AUG-2004
LOCUS AGENCOURT_30842625 NIH_MGC_146 Homo sapiens cDNA clone
DEFINITION

```

FEATURES

IMAGE:7389774 5', mRNA sequence.
 CO959034
 VERSION CO959034.1 GI:51323616
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 721)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 National Cancer Institute / NIH
 Bidg. 31 RM10A07 Bethesda, MD 20892
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Guthrie cDNA Resource Center
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
 cDNA Library Arrayed by: Agencourt Bioscience Corporation
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: IRB18 row: a column: 04
 High quality sequence start: 2
 High quality sequence stop: 328.
 Location/Qualifiers
 1..721
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7389774"
 /tissue_type="mixed"
 /lab_host="DH10B (TI-phage-resistant)"
 /clone_lib="NIH_MGC_146"
 /note="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image/rearrayed_plates/IRBFS.presv.dat
 a. Note: This is a NIH_MGC Library."

Alignment Scores:
 Pred. No.: 1,23e-37 Length: 721
 Score: 480.00 Matches: 93
 Percent Similarity: 83.2% Conservative: 16
 Best Local Similarity: 71.0% Mismatches: 22
 Query Match: 23.4% Indels: 0
 DB: 8 Gaps: 0

US-10-626-445-8 (1-391) x CO959034 (1-721)

Oy 1 MetSerGluSerAsnSerThrGlyLeuProProAlaAlaGlnValProLeuAlaPhe 20
 Db 22 ATGCAGATACATAAGCACAAATTTATACACAGCACTCGTGTACTTTAGCATTT 81

Oy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
 Db 82 TTTATGTCCTTAGTAGCTTTTGGCTATATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 141

Oy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
 Db 142 GTGGTGACAAACCTTAGACATCGAAGTAGTATTTTCTTAAGTGGCATCTCT 201

Oy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
 Db 202 GACTTCTTTGTGGGTGATCTCCATTCCTTTGTACATCCCTCACAGCGTGTTCGAATGG 261

Oy 81 AsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
 Db 262 GATTTTGGAAAGGAATCTGTATTTTGGCTCACTACTGCTATCTGTTATGACCGCA 321

Oy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
 Db 322 GCTGTATATAAGATGTCTCATCAGCTATGATAAATACCTGCTCAATCTCAAAATGCTTTG 381

Oy 121 SerTyrArgAlaGlnHisThrGlyIleMetLys 131
 Db 382 TCTTATGGAACGCAAAAACCGGGGGCGCTGAAG 414

RESULT 6
 LOCUS DA728518 755 bp mRNA linear EST 11-NOV-2005
 DEFINITION DA728518 NT2RM2 Homo sapiens cDNA clone NT2RM2001941 5', mRNA sequence.
 ACCESSION DA728518
 VERSION DA728518.1 GI:81799719
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 755)
 AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fuji, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 HRI human cDNA project: 5' - & 3' - end one pass sequencing: Helix Research Institute (HRI); cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and HRI.

FEATURES
 source Location/Qualifiers
 1..755
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RM2001941"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /clone_lib="NT2RM2"
 /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"

ORIGIN
 Alignment Scores:
 Pred. No.: 3.18e-35 Length: 755
 Score: 456.50 Matches: 112
 Percent Similarity: 50.7% Conservative: 40
 Best Local Similarity: 37.3% Mismatches: 87
 Query Match: 22.3% Indels: 62
 DB: 9 Gaps: 9

US-10-626-445-8 (1-391) x DA728518 (1-755)

Oy 59 IleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPhe 78

```

Db      1 ATCTCCGACTTCTCGTGGCGCTTCTGCAATCCACCTGATGACCTACCTAGCTGCTGACA 60
Qy      79 ---AsnTrpAanPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeu 97
Db      61 GGCGCTGGACCTTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTG 120
Qy      98 CysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117
Db      121 TGCACCTCTCTGCTTCAACATCGTGGCCATCAGTACGACCGCTCTCTGTCGGTCAAC 180
Qy      118 AsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetVal 137
Db      181 CGAGCGTCTCATACCGGGCCACGAGGTACACGCGGGCGGAGTGGCGGAAGATGCTG 240
Qy      138 AlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrp 157
Db      241 CTGTGTGGTGTGGCTTCTCTGCTGACGACGACCATCTCTG-----AGCTGG 291
Qy      158 Lys-----AsnSerThrAsnThrLysAspCysGluProGlyPheValThr 172
Db      292 GAGTACCTGTCGGGGGAGCTTCATCCCCGAGGCGCACTGCTATGCCGAGTTCTTCTAC 351
Qy      173 GluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSerVal 192
Db      352 AACTGTACTTCTCATCAGGCTTCACCTGGAGTCTTTACGCGCTCTCTCCTCAGCGTC 411
Qy      193 AlaTrpPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAlaLeuSerArgCys 212
Db      412 ACCTTCTTAACTCAGCATCTACTGAACATCCAGAGCGC-----ACCGCCT- 461
Qy      213 ProSerHisAlaGlyPheSerThrThrSerSerAlaSerGlyHisLeuHisArgAla 232
Db      462 CCG-----GCT 467
Qy      233 GlyValAlaCysArgThrSerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSer 252
Db      468 GGATGGGGCTGAGAGGAGCCGCGCC----- 494
Qy      253 GluSerProArgLysSerSerIleLeuValSerLeuArgThrHisMetAsnSerSer 272
Db      495 CGAGCCCCCTCCGAGGCCAGCCCTC-----ACCACC 527
Qy      273 IleThrAlaPheLysVal-GlySerPheTrpArgSerGluSerAlaAlaLeuArgGlnAr 292
Db      528 CCCACCGCTGGCTGCTGGGGCTGCTGGCAGAGGGGCGACGGGAGGCCATGCGCGTGCA 587
Qy      292 gGluTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSe 312
Db      588 C-----AGAAAGTGGCCAAGTCTGCGCAGAGGGGCGACGGGCGGCGGCGTGCAG 623
Qy      312 rAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTrpPr 332
Db      624 CATCTTTGGGCTGCTGCTGGGCCCCATACACGCTGCTGATCATCATCGGCGCGNCTGCAT 683
Qy      332 oArgThrGluArgProLysSerValTrpTyr-SerIleAlaPheTrpLeuGlnTrp 350
Db      684 GGCCACTGCTGCCCT---GACTACTGGTACCAAAACCTTCTTCTGCTGCTGCTG 736

RESULT 7
DA308555 558 bp mRNA linear EST 30-OCT-2005
LOCUS DA308555 BRHIP2 Homo sapiens cDNA clone BRHIP2025783 5', mRNA
DEFINITION sequence.
ACCESSION DA308555
VERSION DA308555.1 GI:78290625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 558)

```

AUTHORS Kimura, K., Wakanatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, K., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRHIP2025783"
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/clone_lib="BRHIP2"
/notes="Vector: pME18SFL3"

ORIGIN
Alignment Scores:
Pred. No.: 3,94e-35 Length: 558
Score: 453.50 Matches: 93
Percent Similarity: 65.6% Conservative: 25
Best Local Similarity: 51.7% Mismatches: 53
Query Match: 22.1% Indels: 9
DB: Gaps: 3

US-10-626-445-8 (1-391) x DA308555 (1-558)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 26 CTGGCGCGCTCATGGCGCTCTCATCGTGGCCACGCTGTGGGCAACGGCGTGTGTCATG 85
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 86 CTGCGCTTCGTGGCGGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 145
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 146 GCATCTCCGACTCTCTCGTGGGCGCTTCTGATCCCTGATGATGATGATGATGATGATG 205
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 206 ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTGAGTGTGACTACCTG 265
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 266 CTGTGCACTCTCTCTGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTCTGCTGCTG 325
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
Db 326 ACCGAGCGGTCTCTATACCGGGGCCACAGGGGTGACACGGCGGCGGAGTGGCGGAAGATG 385
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 386 CTGCTGTGTGGTGTGGCTTCTCTGCTGTACGGACCGACCTCTG-----AGC 436

/clone="BRHIP2023706"
/tissue_type="hippocampus"
/clone_lib="BRHIP2"
/note="Vector: pME185FL3"

ORIGIN

Alignment Scores:
Pred. No.: 1.12e-32 Length: 574
Score: 429.50 Matches: 86
Percent Similarity: 64.7% Conservativity: 24
Best Local Similarity: 50.6% Mismatches: 51
Query Match: 21.0% Indels: 9
DB: 3 Gaps: 3

US-10-626-445-8 (1-391) x DA306992 (1-574)

Qy 46 LeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGly 65
Db 1 CTCGGCACCAGACAACTTCTCTGCTCAACTCGCCATCTCGACTTCTCGTGGC 60
Qy 66 LeuLeuSerIleProLeuTyrIleProHisValLeuPhe---AsnTrpAsnPheGlySer 84
Db 61 GCCTTCTGCATCCCACTGATGTACCTACCTGTGTGACAGCGCGCTGGACCTTCGGCGG 120
Qy 85 GlyIleCysMetPheTrpLeuLeuThrAspTyrIleLeuLeuCysThrAlaSerValTyrAsn 104
Db 121 GGCCTCTGCAAGCTGTGGTGTGTAGTGAGTACCTACCTGTGTGACCTCTCTGCCCTTCAAC 180
Qy 105 IleValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAla 124
Db 181 ATCGTGCTCATCAGTACGACCGCTTCTGTGCTGACCGAGCGGTCTCATACCGGCC 240
Qy 125 GlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPhe 144
Db 241 CAGCAGGCTGACACGCGCGGCGAGTGGGAAGATGTGCTGTGGTGTGGCTGCTGCCTTC 300
Qy 145 LeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLys-----Asn 159
Db 301 CTGCTGTACGAGCAGCAGCATCTCTG-----AGCTGGGAGTACCTGTGCGGGGCGAGC 351
Qy 160 SerThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIle 179
Db 352 TCCATCCCCGGGGCCACTGCTATGCGGAGTCTTCTACAACTGGTACTCTCTCATCAGC 411
Qy 180 ThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaIlePheAsnValGlnIle 199
Db 412 GCTTCCACCTGGAGTCTTTACGCCCTCTCTCAGCGTCACTTCTTTAACCCTCAGCATC 471
Qy 200 TyrTrpSerLeuTrpLysArgArgAlaLeu 209
Db 472 TACCTGAACATCCAGCGCGCCAGCCGCGCTC 501

RESULT 10
DW576242 542 bp mRNA linear EST 17-JAN-2006
LOCUS EST ssal_rgb2_40661_rgb2_Salmo_salar cDNA clone
DEFINITION ssal_rgb2_566_015_rev 5', mRNA sequence.

ACCESSION DW576242.1 GI:85048064
VERSION EST.
KEYWORDS Salmo salar (Atlantic salmon)
SOURCE Salmo salar
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

1 (bases 1 to 542)
REFERENCE Koop,B.F., Davidson,W.S. and cGRASP Consortium.
AUTHORS Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
JOURNAL Unpublished (2006)
COMMENT Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada

Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoo@uvic.ca
Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.
Marra. Bioinformatics: Centre for Biomedical Research, University
of Victoria Jong Leong, BF Koop.
Insert Length: 542 Std Error: 0.00
Plate: 586
Seq primer: M13 Reverse
High quality sequence stop: 542.
Location/Qualifiers
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/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clones="ssal_rgb2_566_015_rev"
/tissue_type="mixed tissue"
/clone_lib="rgb2"
/note="Organ: brain, kidney, spleen; Vector: pCMVSPORT6;
ssalrgb2 mixed tissue Salmo salar cDNA; Tissue
contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN

Alignment Scores:
Pred. No.: 4.63e-32 Length: 542
Score: 423.00 Matches: 90
Percent Similarity: 64.7% Conservativity: 22
Best Local Similarity: 52.0% Mismatches: 51
Query Match: 20.7% Indels: 10
DB: 4 Gaps: 4

US-10-626-445-8 (1-391) x DW576242 (1-542)

Qy 45 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuVal 64
Db 1 AGCCTAGCAATCAAGCAACTACTTCTTCTCAACCTTGCCATTTGAGATTTCTGTT 60
Qy 65 GlyLeuLeuSerIleProLeuTyrIleProHisValLeuPhe---AsnTrpAsnPheGly 83
Db 61 GGTGCATTCTGTATCCCTGTATATACCTCCCTACAACTCAGACGCGCTGGTGGTGGC 120
Qy 84 SerGlyIleCysMetPheTrpLeuLeuThrAspTyrIleLeuLeuCysThrAlaSerValTyr 103
Db 121 AGAGGTCTCTGTAAAGCTGTGGCTCTCATGAGTACTTGTCTGACCTGCTGCTTC 180
Qy 104 AsnIleValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArg 123
Db 181 AACATAGTCTCTATCAGCTATGACCGTTCCTCTCCGTACCAGAGCAGTGAATATAGA 240
Qy 124 AlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAla 143
Db 241 GCTCAGCGGAGCATGACCCACCACCTGCTGTGTGAAGATGGTGGTGTGTGGTGGC 300
Qy 144 PheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrp-----Lys 158
Db 301 TTCCTTCTCTATGGCCCTGCGCATTCATC-----TTCTGGAGCTGGTGTGGTGA 351
Qy 159 AsnSerThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThr 178
Db 352 AGCATCTCTGCGCGAGAGTGTTCGCTGAGTGTCTACTGCACTGGTACTTCTCTATC 411
Qy 179 IleThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaIlePheAsnValGln 198
Db 412 AGTCGGTCTACGTTTGAGTTCTTCCACCCCTTTATCTCTGTGACCTTCTTCAACCTG 471
Qy 199 IleTyrTrpSerLeuTrpLysArgArgAlaLeuSerArg 211
Db 472 ATCTACCTGAACATC---CAGAGGAGGAGCAAGAGCAGG 507

RESULT 11
DT257276 728 bp mRNA linear EST 18-AUG-2005
LOCUS DT257276


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DEFINITION JGI CAU08039.fwd CAU Pimephales promelas brain 7-8 month adults,
            males and females pooled (L) Pimephales promelas cDNA clone
ACCESSION  CAU08039 5', mRNA sequence.
VERSION     DT257276
SOURCE      DT257276.1 GI:73559225
ORGANISM    Pimephales promelas
            Pimephales promelas
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Pimephales.
            1 (bases 1 to 728)
AUTHORS     Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
            DOE Joint Genome Institute Pimephales promelas EST project
            Unpublished (2005)
TITLE       Other ESTs: JGI CAU08039.rev
JOURNAL     Contact: Lindquist,E.A., Richardson,P.
COMMENT     DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5800
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            CDNA Library Preparation: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute; http://www.jgi.doe.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone id and the direction of sequencing. The suffix '.fwd'
            indicates a forward sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Plate: CAU0801 row: n column: 18
            High quality sequence stop: 706.
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            /clone_lib="CAU Pimephales promelas brain 7-8 month
            adults, males and females pooled (L)"
            /note="vector: pCMVSPORT6; The library was made from dt
            primed cDNA and cloned into Invitrogen vector pCMVSPORT6.
            Poly A RNA were primed with an oligo dt primer (5'-
            GACTAGTCTAGATCGGACGGCGCGCCCTTTTCTTTT-3') ligated
            to a SalI adapter (5'- TCGACCCAGGCTCCG and 5'-
            CGGACGGGTGG) and digested with NotI. cDNA was size
            selected using 1.1% agarose gel electrophoresis (L
            -0.5-1.2k, M -1.2-2.5k, H ->2.5k) then ligated into NotI
            and SalI digested pCMVSPORT6 vector. The work was done at
            DOE Joint Genome Institute."
ORIGIN
Alignment Scores:
Pred. No.: 3.81e-31 Length: 728
Score: 416.00 Matches: 81
Percent Similarity: 71.9% Conservative: 29
Best Local Similarity: 52.9% Mismatches: 39
Query Match: 20.3% Indels: 4
DB: 10 Gaps: 2

US-10-626-445-8 (1-391) x DT257276 (1-728)

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Qy 28 AlaTleMetValGlyAsnAlaValAlaValleLeuAlaPheValValAsnLeuArg 47
Db 317 GCCACGGTTCGGGAACGCCCTGTGCTATTTAGCTTTTGGTGGAGAAAGTTTACGC 376
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Db 377 ACACAGGGCAACTTTTCTTTTAAATTTGGCCATAGCGGACTTCTTGTGCGTGGTTT 436
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Db 437 TGCATCCCCGTGTATATTCCTTATGCTTACCGGGTGAGTGGAGGCTGGGACAGGTCGT 496
Qy 87 CysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleVal 106
Db 497 TGTAACCTGTGGCTGGTGGTGGATTACATGTTGTGCACCTGCTCAGTCTTCAACATCGT 556
Qy 107 LeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGlnHis 126
Db 557 CTCATCAGTTTCGACAGGTTTCAGTCCGTCACATAAAGCGGTGAGTTACCATTCGCAAAAG 616
Qy 127 ThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal 146
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Qy 147 AsnGlyProMetIleLeuAlaSerAspSerTrpLysAsn 159
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RESULT 12
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DEFINITION CB556920 672 bp mRNA linear EST 02-APR-2003
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ACCESSION CB556920
VERSION    CB556920.1 GI:29496320
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE  1 (bases 1 to 672)
AUTHORS    Angen EST Program.
TITLE      Angen Rat EST Program
JOURNAL    Unpublished (2003)
COMMENT    Contact: Dan Fitzpatrick
            Angen, Inc
            One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00001 row: d column: 6.
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Score: 415.00 Matches: 82
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Best Local Similarity: 57.7% Mismatches: 34
Query Match: 20.3% Indels: 4
DB: 4 Gaps: 2

US-10-626-445-8 (1-391) x CB556920 (1-672)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
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Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 287 CTCGCTTCGGTGGCGGATTTCAGGCTCCGCCACCCAGAACAACTTCTTCTCTCACTC 346

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Db 407 ACCGGCCGTTGACCTTCGGCGGGGCTCTGCAAGCTGTGCTGGTGTAGATTACCTA 466

Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspTyrGlnSerVal 116
Db 467 CTGTGTGCTCCTCGCTTCAACATCGTACTCATCAGCTATGACCGATTCTCTGTCAGTC 526

Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 527 ACTCGAGCTGTCTCTCAGGGCCGACGAGGGGACACGACGAGCGGCGCTTCGGAAGATG 586

Qy 137 ValAlaValTTPLeuIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 587 GCACCTGGTGTGGTGTGCTTCTCTGTGTATGGCTTGCATCTG-----AGT 637

Qy 157 TrpLys 158
Db 638 TGGGAG 643

RESULT 13
CR859546
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo.
1 (bases 1 to 2633)
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp459P0517) is available at the RZPD Deutsches
Reisourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459P0517
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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Best Local Similarity: 27.4% Mismatches: 150
Query Match: 20.2% Indels: 90
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US-10-626-445-8 (1-391) x CR859546 (1-2633)
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Db 287 ACGGGCCCTCTGCTGCTAGCCACAGTACAGGCAACCTGCTGGTACTCATCTCTTCAAG 346
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Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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Qy 160 SerThrAsnThrLys-----AspCysGluProGlyPheValThrGluTrp 174
Db 692 CTGGTAGGGGAGCGGACAGTGTAGTGGGAGTGTACATCCAGTCTCTCTCCAGGCC 751
Qy 175 TyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaTyr 194
Db 752 ATCATCACTTTGGCAGCAGCAGCTGCTCTTCTACCTCCCTCTGTACAGTATGTC--- 808
Qy 195 PheAsnValGlnIleTyrSerLeuTrpLysArg-----ArgAlaLeu 209
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 AK138282
 LOCUS
 DEFINITION
 AK138282 2967 bp mRNA linear HTC 21-SEP-2005
 Mus musculus adult male hypothalamus cDNA, RIKEN full-length
 enriched library, clone:A230054016 product:cholinergic receptor,
 muscarinic 1, CNS, full insert sequence.
 ACCESSION
 VERSION AK138282.1 GI:74209797
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM
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 Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 11076861
 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S.
 and Hayashizaki, Y.
 RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 11217851
 5
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 FANTOM Consortium
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420 (6915), 563-573 (2002)
 12466851
 6
 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C.,
 Maeda, N., Oyama, K., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R.,
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Db 1714 AGAACCCTATGG---GAGCTGGGCTACTGGCTTGTAGTCAACAGCAGCTGTCAACC 1770
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QY 377 lThrLysTrp 380
Db 1828 CTGCGCGTGG 1837

RESULT 15
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LOCUS Mus musculus adult male corpus striatum cDNA, RIKEN full-length
DEFINITION enriched library, clone: C030026C22 product: MUSCARINIC ACETYLCHOLINE
RECEPTOR M1, full insert sequence.
ACCESSION AK081248
VERSION AK081248.1 GI:26349070
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to
PUBMED prepare full-length cDNA libraries for rapid discovery of new genes
REFERENCE Genome Res. 10 (10), 1617-1630 (2000)
AUTHORS 3
11042159
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Matsuda, E., Matakaki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Tanaka, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
FUNCTIONAL annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The PANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6
RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the PANTOM Consortium.
Antisense Transcription in the Mammalian Transcriptome
Science 309, 1564-1566 (2005)
7
The PANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)
8 (bases 1 to 3816)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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SUMMARIES

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ALIGNMENTS

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; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414.010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

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US-10-626-445-8 (1-391) x US-09-414-010-1 (1-1173)

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; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
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Alignment Scores:
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Percent Similarity: 78.3% Conservative: 40
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Query Match: 66.9% Indels: 3
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US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)

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Db 61 TTTATGTCTTCTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCAATTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGTGGACAAACCACTTAGACATCGAAGTAGTATATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPheGlySerGlyIleCysMetPheTrpLeuIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTTGTGGGTGTGATCTCATTTCTTTGTACATCCCTCACAGCTGTTCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleProHisValLeuPheAsnTrp 100
Db 241 GATTTTGGAAAGGAATCTGTGTATTTTGGTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATGATACCTGTGAGTCTCAAAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTTGTACTCTGATGGTGGCGGCTTGG 420
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Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCTTCTTAGTGAATGGGCCCAATGATCTTAGTTTCAGAGTCTTGGGAAGATGAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGGAATGGTATACCTCTTGCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaIlePheAsnValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTATCCCATCTTCTTAGTCTGCTTATTTCAACATCAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCTGTGGAACGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGACTGACTGCT 654
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCCAACACTCTGGGACACTCATTCAGAGGTAGATCATCTTCAAGGAGATCTCT 714
Qy 241 ProGlyLeuLysGluSerAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCCTGCTATCTCTTCAATTCAGAGACAGAGAGAGAGTAGT 774
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTGATGTTTCTCCTCAAGAACCAAGATGAATAGCAATCAATGCTTCCAAATGGGTTC 834
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTrpAlaGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCGTAGCTCTTCCACAAAGGACATGTTGAACCTCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTCTTGTCTGTTTGTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTCTCTGTTCACAAATGTCTTCAATTTATTCTTCAGAACAGGTCCTCAATACAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGATTTGATTTTGGCTTCAGTGGTTCATTTCCCTTTGTCATCTCTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTACAGCGCTTCCAAAGGCTTCTTGAAATATTTTGTATAAAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACAACAGTCGGTCAAGTATCTTCT 1170
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RESULT 3
US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Alignment Scores:
Pred. No.: 5,57e-133 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: Gaps: 2

US-10-626-445-8 (1-391) x US-09-875-076-13 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAATAGCACAAATCAATTTATCACTAGCACTCGTGTACTTACGATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTCTAGTAGCTTTTGTCTATAATCTAGGAAATGCTTTGGTCAITTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTTGGTGGTGTGATCTCAATTCCTTTGTACATCCCTCACAGCTGTTCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGATCTATCTGTATTGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATCTAGGGGTCTGAAGATCTTACTCTGATGGTGGCGGTGTG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 GTGCTGCGCTTCTTAGTGAATGGCCAAATGATCTTAGTTTCAGAGCTCTTGAAGGATGAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAnValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGTGATCCCACTCATCTTAGTCGCTTATTTTCAACATGAAATATTAT 594
Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCTGTGGAGCTGTATCATCTCAGTAGTGCCAAAGCCATCTCGACTGACTGCT 654
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGACTCTCT 714
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCCTGCATCTCTTCAITTCAGAGAGACAGAGGAGAAAGAGTAGT 774
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCAATGTTTCTCACAAGCAACAGATGAATAGCAATCAATGCTTCCAAATGGGTTC 834
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAAGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGCTGTTGCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTCTCTGTTCAATGTTCCTTCAATTTATTTCTCAGCAACAGGCTCTTAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCATTTTGGCTTCACTGTTCAATTCCTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGCGCTTCTTGAATAATTTTGTATAAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTTACCATCAACACACAGTCGGTCAATCTTCT 1170

RESULT 4
US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Alignment Scores:
Pred. No.: 5,6e-65 Length: 2665
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 3 Gaps: 12

US-10-626-445-8 (1-391) x US-09-949-016-5059 (1-2665)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
Db 400 CTGCCCGCTCATGGCGCTGCTCATCTGTCGCCACGGTGTGGCAACGGCGTGTCTCATG 459
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 460 CTGCCCTTCGTGGCGACTCGAGCTCGCACCCAGAACAACTTCTTCTGCTCAACCTC 519
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 520 GCCATCTCCGACTTCTCTGTCGGCGCTTCTGCTATCCACTGTATGATGACCTACGTCGTG 579
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 580 ACAGGCGCTGGACCTTCGGCCGGCGCTCTGCAAGCTGTGGCTGTGGTGTGACTACTG 639
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 640 CTGTGCACCTCTCTGCTTCAACATGCTCATCAGCTACGACCGCTTCTCTGCTGCTG 699
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 700 ACCCGAGCGGTCTCATACCGGGCCAGCAGGGTGACACGGCGGGGCGAGTGGCGAAGATG 759
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 760 CTGCTGTGTGGGTGCTGGCTTCTCTGCTGTACGGACCGACCATCCG-----AGC 810
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 811 TGGGAGTACCTGTCCGGGGGCGAGCTCCATCCCGAGGGCCAGCTGCTATGCGAGTCTTC 870
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 871 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCTGTGAGTTCTTTACGCCCTTCTCAGC 930
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 931 GTACCTTCTTTAACTTCAGCATCTACCTGAACATCCAGAGGCGCACCCGGCTCCGGCTG 990
Qy 200 ----- 200
Db 991 GATGGGCTCGAGAGGCGAGCGGCCCGAGCCCTCCCGAGGGCCAGCCCTCACCACCC 1050
Qy 201 -----TrpSerLeuTyrIleArgAlaLeuSerArgCysProSerHis 215
Db 1051 CCACCGCTGTGCTGTGGGCTGTCTGGCAGAAAGGGGCACGGGGAGGCCATCGCGCTGCAC 1110
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1111 AGTATGGGTGGGTGAGGGCGCGTAGGCGCTGAGGCGCGGGGAGGCGCACCTCGGGGT 1170
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Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1171 GCGCGTGGGGC-----GGTCCGCTGCTTCCACCACCTCCAGCTCCGGC--- 1215
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1216 -----AGTCTCTGAGGGGCACTGAGAGCGCGC----- 1245
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1246 -----TCACTCAAGAGGGGCTCCAAAGCCGCTG 1272
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1273 GCGTCTGCTGGGCCCCATACACGCTGTGTATGATCATCGGGCGCGCTGCCATGGCCAC 1332
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1333 TTTCCGGTGTCTCGGCACAGAAAGTGGCCAGTGGTGGCCGTCATCGTGAGGATCTTT 1392
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1393 GGGCTCTGCTGGGCCCCATACACGCTGTGTATGATCATCGGGCGCGCTGCCATGGCCAC 1452
Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1453 TGCCTCCCT---GACTACTGTGTACGAAACCTCTTCTGGCTCTGTGGGCCAACTCGGCT 1509
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1510 GTCAACCTGTCTTACCTCTGTGTCACACACAGTTCGCCGGGCTTCACCAAGCTG 1569
Qy 375 LeuCysValThrLys-----Trp----- 380
Db 1570 CTCTGCCCCCAGAGCTCAAAATCCAGCCACAGCTCCCTGGAGCACTGTCTGAAGTGA 1629
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1630 GTGGCCCCCAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCAGGCTCT 1677
RESULT 5
US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/985,090
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
```

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-08-985-090-1

Alignment Scores:
Pred. No.: 5.68e-65 Length: 2689
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 2 Gaps: 12

US-10-626-445-8 (1-391) x US-08-985-090-1 (1-2689)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
Db 399 CTGGCCGCGTCTATGGCGCTGCTCATCTGGCCACGGTGTGGGCAACGCGCTGGTCAATG 458
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 459 CTGGCTTCGTGGCGGACTCGAGCTCCGACCCAGAACAACTTCTTCTCTCTCAACCTC 518
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 519 GCCATCTCCGACTTCTCTCGCGCGCTTCTGCACTCCACATGATGATACCTACGTGCTG 578
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 579 ACAGCCGCTGGACCTTCGGCCGGGCTCTGCAAGCTGTGGTGTAGTACGTACCTG 638
Qy 97 LeuCysThrAlaSerValTyrAsnIleValIleLeuSerTyrAspArgTyrGlnSerVal 116
Db 639 CTGTGACCTCTCTGCTTCAACATCGTGTATCATAGTACGACCGCTTCTCTCGGTC 698
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 699 ACCGAGCGGTCTCATACCGGGCCACAGGGTGACACGGCGCGGCGAGTCCGGAAGATG 758
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 759 CTGCTGTGTGGGTGTGGCTTCTCTGTCTGACGACCGACCATCTCTG-----AGC 809
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 810 TGGAGTACCTGTCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTC 869
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 870 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCCCTGGAGTCTTTTACGCCCTCTC 929
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 930 GTCACTTCTTTTAACTCTCAGCATCTACTGAACTCCAGAGGGCGACCCGCTCGGGCTG 989
Qy 200 ----- 200
Db 990 GATGGGCTCGAGAGGCGAGCGCGCCCGAGCCCTCCCGAGGGCCAGCCCTCACCACCC 1049
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 1050 CCACCGCTCGCTGTGGGCTGTCTGCGAAGAGGGCGACCGGGAGGCCATCCCGCTGCAC 1109
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1110 AGGTATGGGTGGGTGAGGGCGCGTAGGCGCTGAGCGCGGGAGGAGCGACCTCGGGGT 1169
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Db 1110 AGGTATGGGTGGGTGAGCGCGCTAGGCGCTGAGCGCGGAGGCGACCTCGGGGT 1169
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1170 GCGGTGGGGC-----GGCTCCGTGGCTTCAACCACTCCAGCTCCGGC--- 1214
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1215 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 1244
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1245 -----TCACTCAGAGGGGCTCAAGCCGTCG 1271
Qy 284 SerGluSerAlaLeuArgLysArg-----GluTyr 294
Db 1272 GCGTCTCGGCTCACTCGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCAACCCAGCGC 1331
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1332 TTTCGGCTGTCTCGGACAGAAAGTGGCCAAAGTCGCTGGCGGTCATCGTGAGCATCTTT 1391
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1392 GGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGCGCGCTGCCATGGCCAC 1451
Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1452 TGCCTCCT---GACTACTGGTAGCAAACTCTCTGGCTCTCTGGGCCAACTCGGCT 1508
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1509 GTCAACCTCTCTCTACCTCTGTGCCACACAGCTTCGCGCGGCTTCAACCAAGCT 1568
Qy 375 LeuCysValThrLys-----Trp----- 380
Db 1569 CTCTGCCCCCAGAGCTCAAAATCCAGCCACAGCTCCCTCGGAGCACTGCTGAAGTGA 1628
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1629 GTGGCCCAACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCAGGTCT 1676

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RESULT 7

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US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-5

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Alignment Scores:

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Pred. No.: 5,72e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115

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DB: 3 Gaps: 12
US-10-626-445-8 (1-391) x US-09-167-354-5 (1-2699)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 407 CTGGCGCGCTCATGGCGCTGCTCATCGTGGCCACGGTGTGGGCGACGGCGTGGTCTCATG 466
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTCGCCCTTCGTGGCGCACTCGAGCTCCGACCCAGAACCAACTTCTTCTCTCTCAACCTC 526
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 527 GCCATCTCCGACTTCTCTGTCGGCGCTTTCGATCCCACTGTATGATCCCTCATGTCGTG 586
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 587 ACAGGCGCTGGACCTTTCGGCCGGGGCTCTGCAAGCTGTGGTGGTAGTGGACTACCTG 646
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGCACCTCTCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTCTGTCTGCTC 706
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 707 ACCGAGCGGTCTCATACCGGGGCCACAGGGTGACACGGCGGGCGGAGTGGCGGAAGATG 766
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 767 CTGCTGTGTGGGTGTGGCTTCTCTGCTGTACGACCGACCATCTCTG-----AGC 817
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 818 TGGAGTACCTGTCCGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCCAGTCTCTTC 877
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 878 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCTGGAGTCTTTTACGCCCTCTCTCAGC 937
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 938 GTACACTTCTTTAACTCAGCATCTACTGAACATCCAGAGGGCGACCCGCGCTCGGGTGTG 997
Qy 200 ----- 200
Db 998 GATGGGCTCGAGAGGCGAGCGCGCCCGAGCCCTCCCGAGGCCAGCCCTCACCACCC 1057
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 1058 CCACCGCTCGCTGTGGGCTGCTGGCAGAGGGGCGACCGGGAGGCGCATGCCGCTGCAC 1117
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1118 AGGTATGGGTGGGTGAGCGCGCTGAGCGCTGAGCGCGGGAGGCGACCTCGGGGT 1177
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1178 GGGCGTGGGGC-----GGCTCGGTGGCTTCAACCCACCTCAGCTCCAGCTCCGGC--- 1222
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1223 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 1252
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1253 -----TCACTCAGAGGGGCTCAAGCCGTCG 1279
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1280 GCGTCTCGGCTCTGCTGGAGAGCGCATGAAGATGGTGTCCCAGAGCTTCAACCCAGCGC 1339
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314

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Db 1340 TTTCCGGCTGCTCGGGACAGAAAGTGGCAAGTGGCTGGCGTCATCGTAGGCACTCTT 1399
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1400 GGGCTCTGCTGGGCCCATACACGCTCTGATGATCATCCGGCCGCTGCCATGGCCAC 1459
Qy 335 GluArgProLysSerValTyrTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPhe 354
Db 1460 TGGCTCCCT---GACTACTGGTAGAAACCTCTCTTGGCTCTCTGGTGGCCAACTCGGCT 1516
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1517 GTCAACCTCTGCTCTACCTCTCTGTGCCACACAGCTTCCGGCGGGCTTCCACCAAGCTG 1576
Qy 375 LeuCysValThrLys-----ProAlaLeuSerGlnAsnGlnSer 388
Db 1577 CTCTGCCCCCAGAGACTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGA 1636
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1637 GTGGCCCCACAGAGCTCCCTCGACCCAGCGCTCTCTCAGCCCCAGGTCT 1684

RESULT 8
US-09-642-855-5
; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Javashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5

Alignment Scores:
Pred. No.: 5,72e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 3 Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-855-5 (1-2699)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 407 CTGGCCGGCTCATGGCGCTGCTCATCTGTCGCCACCGTGTGGGCCACCGCTGTCATG 466
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTCGCCCTTCGTGGCGGACTCGAGGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 526
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIle 77
Db 527 GCCATCTCCGACTTCTCTGCTGGCGGCTTTCGTGATCCACCTGATGATCCCTACGTGCTG 586
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 1577 CTCTGCCCCCAGAGACTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGA 1636
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Db 587 ACAGGCGCTGGACCTTCGGCCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACTCGT 646
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGACCTCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTCTCGGTC 706
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 707 ACCGAGCGCTCTCATACCGGGCCAGCAGGGTGACACGGCGGGGAGTGGGAGATG 766
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 767 CTGCTGGTGGTGGTGGCTTCTCTGCTGATCGGACCAAGCATCTCTG-----AGC 817
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 818 TGGAGTACCTGTCCGGGGGACAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTC 877
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 878 TACAACCTGGTACTTCTCTCATCAGGGCTTCCACCTGGAGTCTTTTACGCGCTCTCTCAGC 937
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 938 GTCACTTCTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 997
Qy 200 ----- 200
Db 998 GATGGGGCTCGAGAGGAGGAGCGCGCGCCCGAGCCCTCCCGAGGGCCAGCCCTCACACCC 1057
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 1058 CCACCGCTGGCTGCTGGGGCTGCTGGCAGAGGGCAGCGGGAGGCATGCGCGCTGCAC 1117
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1118 AGGTATGGGTGGGTGAGGGCGGCTAGGCGCTGAGGCGCGGGAGGCGGCGCTCGGGGGT 1177
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1178 GCGGTGGGGG-----GGCTCGTGGCTTCAACCACCTCCAGCTCGGCG----- 1222
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1223 -----AGCTCTCGAGGGGCACTGAGAGCGCGCG----- 1252
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1253 -----TCACTCAAGAGGGGCTCCAAAGCGCTCG 1279
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1280 GCGTCTCGGCTCGCTGGAGAGCGCATGAGATGTTGTGCCAGAGCTTACCCAGCGC 1339
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1340 TTTCCGGCTGCTCGGGACAGAAAGTGGCCAAAGTGGCTGCGCTGTCATCGTAGGATCTTT 1399
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1400 GGGCTCTGCTGGGCCCATACACGCTCTGATGATCATCCGGCCGCTGCCATGGCCAC 1459
Qy 335 GluArgProLysSerValTyrTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPhe 354
Db 1460 TGGCTCCCT---GACTACTGGTAGAAACCTCTCTTGGCTCTCTGGTGGCCAACTCGGCT 1516
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1517 GTCAACCTCTGCTCTACCTCTCTGTGCCACACAGCTTCCGGCGGGCTTCCACCAAGCTG 1576
Qy 375 LeuCysValThrLys-----Trp----- 380
Db 1577 CTCTGCCCCCAGAGACTCAAAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGA 1636
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Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1637 GTGCCCCACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCAGGTCT 1684

RESULT 9
US-09-642-514-5
; Sequence 5, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5

Alignment Scores:
Pred. No.: 5,72e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 3 Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-514-5 (1-2699)
Qy 18 LeuAlaPheLeuMetSerPheAlaPheAlaMetValGlyAsnAlaValVal 37
Db 407 CTGCCCGGCTCATGGCGCTGCTCATGTGGCCAGCGTGTGGCAGCGCTGTCATG 466
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTCGCTTCGTGGCGGACTCGAGGCTCCGCCACCAGAACAACTTCTTCTGCTCAACCTC 526
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 527 GCCATCTCCGACTTCTCTGTCGGCGGCTTCTGCAATCCCACTGTATGTACCTACGTGCTG 586
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 587 ACAGGCGCTGGACCTTCGGCGCGGCGCTCTGCAAGTGTGGTGGTAGTGAGTACTCTG 646
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGCACCTCTCTGCTTCAACATCGTGTCTCATAGCTACGACCGCTTCTCTGCGTCTC 706
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
Db 707 ACCCGAGGGTCTCATACCGGGCCAGCAGGGGTACACCGCGCGCGGCGAGTGGCAAGATG 766
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 767 CTGTGTTGGTGGTCTCTCTGCTTCTCTGCTACGACCGACCATCTCTG-----AGC 817
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 818 TGGGAGTACCTGTCCGGGGGCGAGCTCCATCCCGGAGGCCACTGCTATGCGAGTCTTCTC 877
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Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 878 TAAACTGGTACTTCTCTCATCACCGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCAGC 937
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 938 GTCACTTCTTTAACTCAGCATCTACTGAACATCCAGAGGCGCACCGCTCCGGCTG 997
Qy 200 ----- 200
Db 998 GATGGGCTCGAGAGGCGAGCGGCCCGAGCCCTCTCCGAGGCCAGCCCTCACCACC 1057
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 1058 CCACCGCTGGTCTGGGGCTGTGGCAGAGAGGGGCGAGGGAGGCATCCCGCTGCAC 1117
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 1118 AGGTATGGGGTGGGTGAGCGCGCGGTAGCGCTGAGCGCGGGGAGGCGCACCTCGGGGGT 1177
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1178 GCGGTGGGGC-----GGCTCGTGGCTTCAACCCACTCCAGCTCCGGC--- 1222
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1223 -----AGCTCTCGAGGGCGACTGAGAGGCGCGC----- 1252
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1253 -----TCACTCAAGAGGGGCTTCAAGCCGCTCG 1279
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1280 GCGTCTCGCGCTCGCTGGAGAGCGCATGAAGATGGTGTCCACAGAGCTTCAACCCAGCGC 1339
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1340 TTTCGGCTGTCTCGGACAGGAAGTGGCCGCTGCTGGCCGCTCATCGTGGAGCATCTTT 1399
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1400 GGGCTCTGCTGGGCGCCATACACGCTCTGATGATCATCCGGCGCGCTGCGCATGGCCAC 1459
Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1460 TGGCTCCCT---GACTACTGTGTACGAAACCTCTTCTGGCTCTCTGGGCGCACTCGGCT 1516
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1517 GTCAACCTCTCTCTTACCTCTGTGCCACACAGCTTCCGCGGGGCTTCAACCAAGCTG 1576
Qy 375 LeuCysValThrLys-----Trp----- 380
Db 1577 CTGTGCCCCCAGAGCTCAAAATCCAGCCACAGTCCCTGGAGAGCTGCTGGAAGTGA 1636
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1637 GTGCCCCACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCAGGTCT 1684

RESULT 10
US-09-642-852-5
; Sequence 5, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,852
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; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 05/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-852-5

Alignment Scores:
Pred. No.: 5,72e-65 Length: 2699
Score: 724.50 Matches: 171
Percent Similarity: 48.9% Conservative: 52
Best Local Similarity: 37.5% Mismatches: 118
Query Match: 35.4% Indels: 115
DB: 12 Gaps: 12

US-10-626-445-8 (1-391) x US-09-642-852-5 (1-2699)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
Db 407 CTGGCGCGCTCATGGCGCTCATCGTGGCCACCGGTGTGGGCAAGCGCTGGTCTATG 466
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTGGCGCTTCGTGGCGGCTCGGAGCTCCGACCCAGAACCACTTCTTCTCTGCTCAACCTC 526
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValIle 77
Db 527 GCCATCTCCGACTTCTCTGCGGGCGCTCTGCAATCCACTGTATGATGACCTAGCTGCTG 586
Qy 78 Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeu 96
Db 587 ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAGTACTCTG 646
Qy 97 LeuCysThrAlaSerValTyrAsnIleValIleLeuSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGCACTTCTCTGCTGCTCAACATCGTGTATCAGTACGACCTGCTCTCTCTGCTGCTG 706
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
Db 707 ACCGAGCGGTCTCATACCGGGCCACAGCGGTGACACGGCGGGCGGAGTGGCGAAGATG 766
Qy 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 767 CTGCTGTGTGTGGTGTCTGGCTTCTCTGTGACGACCCAGCATCTCTG---AGC 817
Qy 157 TrpIys-----AsnSerThrAsnThrIysAspCysGluProGlyPheVal 171
Db 818 TGGGAGTACCTGTCTCGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTC 877
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
Db 878 TACACTGTGTACTTCTCTATCAGCGGTTCACCCCTGGAGTCTTTTACGCGCTCTCTCAGC 937
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 938 GTCACCTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGGCACCCTCGCGCTG 997
Qy 200 ----- 200
Db 998 GATGGGCTCGAGAGGACGGCGCCCGAGCCCTCTCCGAGGCCAGCCCTCCACACCC 1057
Qy 201 -----TrpSerLeuTyrIleArgAlaLeuSerArgCysProSerHis 215
Db 1058 CCACCGCTGCTCTCTGGGCTGTGGCAGAAAGGGGACCGGGAGGCGATGCGCTGCAC 1117
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 223 -----AlaGlyPheSerThrThrSerSer 223
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Db 1118 AGGTATGGGTGGTGGTGGCGCGCTAGGCGCTAGGCGCGGGAGGCGAGCCCTCGGGGGT 1177
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 1178 GCGCGTGGGGC-----GGCTCGTGGCTTACCCACCTCCAGCTCCGGC--- 1222
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 1223 -----AGCTCTCTGAGGGGACATGAGAGCGCGGC----- 1252
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 1253 -----TCACTCAAGAGGGGCTCCAAAGCCGCTCG 1279
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 1280 GCGTCTCGCGCTCGCTGGAGAGCGCATGAAGATGTGTGCCAGAGCTTCAACCAGCGC 1339
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1340 TTTCCGCTGTCTCGGACAGGAAAGTGGCAAGTGGCTGGCGCTCATCGTGAGCATCTTT 1399
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1400 GGGCTCTGCTGGGCCCCATACACGCTGTATGATCATTCGCGGCGCGCTGCCATGGCCAC 1459
Qy 335 GluArgProLysSerValTyrTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerPhe 354
Db 1460 TGGCTCCCT---GACTACTGTGTAGAAACCTCTCTGTGGCTCTCTGTGGGCAACTCGGCT 1516
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1517 GTCAACCTGTCTCTACCTCTGTGCCACACAGCTTCCGCGGGGCTTCAACCAAGCTG 1576
Qy 375 LeuCysValThrIys-----Trp----- 380
Db 1577 CTCTGCCCCAGAAAGCTCAAAATCCAGCCACACAGCTCCCTGGAGCACTGCTGGAAGTGA 1636
Qy 381 -----ProAlaLeuSerGlnAsnGlnSer 388
Db 1637 GTGGCCACCAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCCGAGGTCT 1684

RESULT 11
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MN1-032
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1335 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1335
 US-08-985-090-3

Alignment Scores:

Pred. No.: 2,89e-65 Length: 1335
 Score: 722.50 Matches: 165
 Percent Similarity: 50.8% Conservative: 51
 Best Local Similarity: 38.8% Mismatches: 116
 Query Match: 35.3% Indels: 93
 DB: 2 Gaps: 10

US-10-626-445-8 (1-391) x US-08-985-090-3 (1-1335)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValle 37
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 Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
 Db 169 CTGGCTTCTGGCGGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 228
 Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValleu 77
 Db 229 GCCATCTCCGACTTCTCTGCTGGCGCTCTGTCATCCCACTGTATGTACCTAGTGTGCTG 288
 Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
 Db 289 ACAGGCGCTGGACCTTGGCGCGGCGCTCTGCAAGCTGTGGTGTAGTGGACTACCTG 348
 Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
 Db 349 CTGTGCACTCTCTGCTTCAACATCTGCTATCATAGCTACGACCCCTCTCTGCTCGCTC 408
 Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
 Db 409 ACCCGAGCGTCTCATACCGGCGCCAGCAGCGGTGACACGCGCGGCGGAGATG 468
 Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
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 Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
 Db 520 TGGAGTACCTGTCCGGGGGAGCTCATCCCGAGGCGCAGTCTGCTATGCGAGTCTTC 579
 Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
 Db 580 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCTCGGAGTCTTTACGCGCTTCTCTCAGC 639
 Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
 Db 640 GTCACCTTCTTTAACTCTAGCATCTACCTGAACATCCAGAGGCGCACCCGCTCCGCGCTG 699
 Qy 200 ----- 200
 Db 700 GATGGGCTCGAGAGGAGCGCGCGCCCGAGCCCTCTCCGAGGCGCCAGCCCTCACCAACC 759
 Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
 Db 760 CCACCGCTGGCTGCTGGGCTGCTGCGACAGGCGCACGGGAGGCGCATGCGCTCCAC 819
 Qy 216 -----AlaGlyPheSerThrThrSerSer 223

Db 820 AGGTATGGGTGGGTGAGGGCGCGTAGGCGCTGAGCGCGGAGGCGACCTCGGGGT 879
 Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
 Db 880 GCGCGTGGGGC-----GGCTCGTGGCTTCAACCACTCCAGCTCCGCGC--- 924
 Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
 Db 925 -----AGCTCTCGAGGGCACTGAGAGGCGCGC----- 954
 Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
 Db 955 -----TCACTCAAGAGGGGCTCCAAGCGCTCG 981
 Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
 Db 982 GCGTCTCGGCTCTCACTGGAGAGCGCATGAAGATGTTGCCAGAGCTTCAACCAAGCGC 1041
 Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
 Db 1042 TTTGCGCTGTCTCGGGACAGGAAAGTGGCCCAAGTGGTGGCGCTCATGTGAGCATCTTT 1101
 Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
 Db 1102 GGGCTCTGCTGGGCGCCCATACGCTGCTGATGATCATCGGCGCGCTGCCATGGCCAC 1161
 Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
 Db 1162 TGGCTCCCT---GACTACTGTAGTACGAACCTCTCTGCTGCTGGCGCACTCGGCT 1218
 Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
 Db 1219 GTCAACCTCTCTCTACCTCTGTGCCACACAGCTTCCGCGCGGCTTCAACAAGCTG 1278
 Qy 375 LeuCysValThrLys 379
 Db 1279 CTCTGCCCCCAGAG 1293

RESULT 12

US-09-165-543-3
 ; Sequence 3, Application US/09165543
 ; Patent No. 6093545
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
 ; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/165,543
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/042,780
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elizabeth A. Hanley
 ; REGISTRATION NUMBER: 33,505
 ; REFERENCE/DOCKET NUMBER: MNI-032CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1335 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..1335
;   US-09-165-543-3

Alignment Scores:
Pred. No.:      2,89e-65      Length: 1335
Score:          722.50
Percent Similarity: 50.8%
Best Local Similarity: 38.8%
Query Match:    35.3%
Indels:         93
Gaps:           10
DB:

US-10-626-445-8 (1-391) x US-09-165-543-3 (1-1335)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValle 37
DB 109 CTGGCCGCGCTCATGGCGTCTCATCGTGCACCGGTGTGGCAAGCGTGTGTCATG 168
QY 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
DB 169 CTGGCTTCTGTGGCGACTCGAGCTCCGACCCAGACCAACTTCTTCTGTCTCAACCTC 228
QY 58 AlaIleSerAspPheLeuValGlyLeuIleSerIlePheLeuTyrIleProHisValLeu 77
DB 229 GCCATCTCCGACTTCTCTGTGGCGGCTCTGATCCCATCTGATGATGATGATGATGCTG 288
QY 78 Phe----AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB 289 ACAGGCGCTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGTGTGAGTGACTACCTG 348
QY 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
DB 349 CTGTGCACCTTCCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTGTGCGGT 408
QY 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
DB 409 ACCGAGCGGTCTCATACCGGGCCACAGCGGTGACACGGCGGGGCGGAGTGCAGAGATG 468
QY 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB 469 CTGCTGTGTGGTGTGCTGCTTCTGCTGTACGACCGACCATCTCTG-----AGC 519
QY 157 TrpIys-----AsnSerThrAsnThrIlysAspCysGluProGlyPheVal 171
DB 520 TGGGAGTACCTGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTC 579
QY 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
DB 580 TACAATGGTACTTCTCTATCAGCGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCAGC 639
QY 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
DB 640 GTCACCTTCTTAACCTCAGCATCTACCTGAACATCCAGAGGGCGACCCCGCTCCGGGTG 699
QY 200 ----- 200
DB 700 GATGGGCTCGAGAGGCGAGCGGCCCGAGCCCTCCCGAGGGCCCGCTCACCAACC 759
QY 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
DB 760 CCACCGCTGCTGCTGTGGAGGTGCTGGCAGAGAGGGGCGCGGGAGGCATGCGCTCCAC 819
QY 216 -----AlaGlyPheSerThrThrSerSer 223
DB 820 AGGTATGGGTGGTGTAGGCGGCGGTAGGCGCTGAGGCGCGGGGAGGCGACCTCGGGGT 879
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QY 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
DB 880 GGGCGTGGGGC-----GGCTCGTGGCTTACCCACCTCCAGCTCCGGC--- 924
QY 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSerIleLeuVal 263
DB 925 -----AGTCTCTCGAGGGGCACTGAGAGCGCGC----- 954
QY 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheIysValGlySerPheTrpArg 283
DB 955 -----TCACTCAAGAGGGGCTCCAAGCCGCTCG 981
QY 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
DB 982 GCGTCTCGGCTCACTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCACCCAGCGC 1041
QY 295 AlaGluLeuLeuArgGlyArgIysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
DB 1042 TTTTCGGCTGTCTCGGGACAGGAAAGTGGCAAGTCTGTCGCGCTCATCGTGAGCATCTTT 1101
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
DB 1102 GGGCTCTGCTGGGCCCATACACGCTGCTGATGATCATCGGGCGCGCTGCCATGGCCAC 1161
QY 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
DB 1162 TGGCTCCCT---GACTACTGGTACGAAACCTCTCTTGGCTCTGTGGGCACTCGGCT 1218
QY 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnIysAlaPheTrpIle 374
DB 1219 GTCAACCTCTGCTCTTACCTCTGTGCCACACAGCTTCGCGCGGGCTTCACCAAGCTG 1278
QY 375 LeuCysValThrIys 379
DB 1279 CTCTGCCCCCAGAG 1293

RESULT 13
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Javashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-167-354-6

Alignment Scores:
Pred. No.:      2,89e-65      Length: 1335
Score:          722.50
Percent Similarity: 50.8%
Best Local Similarity: 38.8%
Query Match:    35.3%
Indels:         93
Gaps:           10
DB:

US-10-626-445-8 (1-391) x US-09-167-354-6 (1-1335)
QY 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValValle 37
DB 1167 ----- 1167
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Db 109 CTGGCCGGCTCATGGCGCTGCTCATCTGGCCACGGTGTGGCAACGGCTGGTCATG 168
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTCGCCCTTCGTGGCGGCTCGGAGCTCGGCAACCCAGAACAACTTCTTCTGCTCAACGCTC 228
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 229 GCCATCTCCGACCTTCTGCTGGCGCTTCTGCAATCCCACTGATGATACCTCATGTCGTG 288
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGCCCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTCGT 348
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTGCTGCTCAACATCGTGTCTCATAGCTACGACCGCTTCTGCTGGTC 408
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 409 ACCCGAGCGGTCTCATACCGGGCCAGAGGGTGACAGCGGGCGGCGAGTCCGGAGAATG 468
Qy 137 ValAlaValTyrPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGGTCTGCTGGCTTCTGCTGTACGACGACGACCTCTG-----AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 520 TGGGAGTACCTGTCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCTTC 579
Qy 172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
Db 580 TACAACCTGGTACTTCTCTCATCAGCGCTTCCACCTCGGAGTTCTTTACGCCCTTCTCAGC 639
Qy 192 ValAlaTyrPheAsnValGlnIleTyr----- 200
Db 640 GTCACTTCTTTAACCCTCAGCATCTACTGACATCCAGAGGCGCACCGCGCTCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGCTCGAGAGCGCAGCGGCCCGAGCCCTCCGAGGCCAGCCCTCACCAACC 759
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHis 215
Db 760 CCACCGCTGCTGCTGGCGCTGTGCGAGAAGGGCAGCGGGAGGCCATGCGCGCTGCAC 819
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 820 AGGTATGGGTGGTGGAGCGCGCTAGGCGCTGAGCGCGGGAGGCGACCTCGGGGGT 879
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 880 GCGGTGGGGC-----GGCTCGGTGCTTCAACCACTCCAGCTCGGC----- 924
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 925 -----AGCTCTCGAGGGCAGCTGAGAGCGCGC----- 954
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 955 -----TCATCAAGAGGGGCTTCAAGCCGTG 981
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 982 CGCTCTCGGCTCGCTGGAGAACGCGCATGAAGATGTGTCCAGAGCTTCAACCCAGCGC 1041
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1042 TTTTCGGCTGTCTCGGAGCAGAAAGTGGCCAAAGTCGCTGGCGCTCATCGTGAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1102 GGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGGCCGCTGCGCATGGCCAC 1161

Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1162 TGCCTCCCT---GACTACTGGTACGAAACCTCTCTTCTGGCTCTCTGGGCCAACCTCGGCT 1218
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1219 GTCNACCTCTCTCTTACCTCTGTGTCACCAACAGCTTCCGCCGGGCTTCCACCAAGCTG 1278
Qy 375 LeuCysValThrLys 379
Db 1279 CTCTGCCCCCAGAAG 1293
RESULT 14
US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6
Alignment Scores:
Pred. No.: 2,89e-65 Length: 1335
Score: 722.50 Matches: 165
Percent Similarity: 50.8% Conservative: 51
Best Local Similarity: 38.8% Mismatches: 116
Query Match: 35.3% Indels: 93
DB: 3 Gaps: 10
US-10-626-445-8 (1-391) x US-09-642-855-6 (1-1335)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 109 CTGGCCCGCTCATGGCGCTGCTCATCTGGCCACCGGTGTGGCAACGGCTGGTCATG 168
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTGCGCTTCGTGGCGGCTCTGCTGGCGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 228
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 229 GCCATCTCCGACCTTCTGCTGGCGCTTCTGCAATCCCACTGATGATACCTCATGTCGTG 288
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGCCCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTCGT 348
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTGCTGCTCAACATCGTGTCTCATAGCTACGACCGCTTCTGCTGGTC 408
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 409 ACCCGAGCGGTCTCATACCGGGCCGAGGGTGACAGCGGGCGGCGAGTCCGGAGAATG 468

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Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGGTCTGGCTTCTGCTGTACGACCGACCATCTTG-----AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 520 TGGAGTAGTCTGTCGCGGGGCGAGCTCCATCCCGAGGCGCACTGCTATCGGAGTTCTTC 579
Qy 172 ThrGluTrpTrpIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
Db 580 TACAACCTGGTACTTCTTCATACCGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCCAGC 639
Qy 192 ValAlaTrpPheAsnValGlnIleTyr----- 200
Db 640 GTACACCTTCTTTAACTTACCTCAGCATCTACTGAACATCCAGAGCGCACCGCGCTCCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGGCTCGAGAGCGACGCGCGCCCGAGCCCTCCCGAGGCGCCAGCCCTCACACCCC 759
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCyeProSerHis 215
Db 760 CCACCGCTGGCTGCTGGGGCTGTGTGCAAGAAGGGGACGCGGGAGGCCATGCCGCTGCAC 819
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 820 AGGTATGGGTGGGTGAGCGCGCGCTAGCGCGCTAGCGCGCGGGAGCGACCTCGGGGGT 879
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 880 GCGCGTGGGGC-----GGCTCCGTGGCTTCAACCCACTCCAGCTCCGGC--- 924
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSerIleLeuVal 263
Db 925 -----AGCTCTCGAGGGGCACTGAGAGCGCGCGC----- 954
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 955 -----TCACTCAAGAGGGGCTCCAGCCCTGCG 981
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTrp 294
Db 982 GCGTCTCGGCTCGCTCGGAGAAGCGCATGAAGATGGTGTCCAGAGCTTCACCCAGCGC 1041
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1042 TTTCCGCTGTCTCGGACAGGAAAGTGGCCAAAGTCGCTGGCGGTCATCGTAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1102 GGGCTCTGTGGGCCCCATACACGCTGTGTATGATCATCCGGGCGGCTGCCATGGCCAC 1161
Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1162 TGCCTCCCT---GACTACTGTGATCGAAACCTCTCTGGCTCTGTGGGCCAACTCGGCT 1218
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1219 GTCAACCCCTGTCCTTACCTCTGTGCCACCAACAGCTTTCGCGCGGGGCTTCACCAAGCTG 1278
Qy 375 LeuCysValThrLys 379
Db 1279 CTCGTCCCCCAGAG 1293
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RESULT 15

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US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
```

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; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,514
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-6

Alignment Scores:
Pred. No.: 2,89e-65 Length: 1335
Score: 722.50 Matches: 165
Percent Similarity: 50.8% Conservative: 51
Best Local Similarity: 38.8% Mismatches: 116
Query Match: 35.3% Indels: 93
DB: 3 Gaps: 10

US-10-626-445-8 (1-391) x US-09-642-514-6 (1-1335)

Qy 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle 37
Db 109 CTGGCCCGCTCATGGCGTCTCATCGTGCCACCGTCTGGGCAACGCGCTGTCATG 168
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTGCGCTTGTGGCGACTCGAGCTCCGACCCAGAACACTTCTTCTCTCTCAACCTC 228
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 229 GCCATCTCCGACTTCTCTCGTGGCGCTTCTGCATCCACTGTATGTACCTACCTGCTG 288
Qy 78 Phe---AsnTrpAsnPheGlySerGlyLeuCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGGCGCTGGACCTTTCGGCCGGGGCTCTGCAAGTGTGGCTGGGTGAGTACCTCG 348
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACTCTCTGCTTCAACATGCTGCTCATAGCTACGACCGCTTCTCTCGGTC 408
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGGCCAGCGGGTGACACGGCGCGGCGGAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGTGTGTGGGTGCTGGCGCTTCTCTGTGTACGACCGACCATCTCTG-----AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
Db 520 TGGAGTAGTCTGTCGCGGGGCGAGCTTCCATCCCGAGGCGCACTGCTATCGGAGTTCTTC 579
Qy 172 ThrGluTrpTrpIleLeuThrIleThrMetLeuLeuGluPheLeuProValIleSer 191
Db 580 TACAACCTGGTACTTCTCTCATCCGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCCAGC 639
Qy 192 ValAlaTrpPheAsnValGlnIleTyr----- 200
Db 640 GTACACCTTCTTTAACTTACCTCAGCATCTACTGAACATCCAGAGCGCACCGCGCTCCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGGCTCGAGAGCGACGCGCGCCCGAGCCCTCCCGAGGCGCCAGCCCTCACACCCC 759
Qy 201 -----TrpSerLeuTrpLysArgAlaLeuSerArgCyeProSerHis 215
Db 925 -----TCACTCAAGAGGGGCTCCAGCCCTGCG 981
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTrp 294
Db 982 GCGTCTCGGCTCGCTCGGAGAAGCGCATGAAGATGGTGTCCAGAGCTTCACCCAGCGC 1041
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1042 TTTCCGCTGTCTCGGACAGGAAAGTGGCCAAAGTCGCTGGCGGTCATCGTAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1102 GGGCTCTGTGGGCCCCATACACGCTGTGTATGATCATCCGGGCGGCTGCCATGGCCAC 1161
Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1162 TGCCTCCCT---GACTACTGTGATCGAAACCTCTCTGGCTCTGTGGGCCAACTCGGCT 1218
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1219 GTCAACCCCTGTCCTTACCTCTGTGCCACCAACAGCTTTCGCGCGGGGCTTCACCAAGCTG 1278
Qy 375 LeuCysValThrLys 379
Db 1279 CTCGTCCCCCAGAG 1293
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Db 760 CCACCGCTGCTGGCTGCTGGCAGAGGGGCACGGGAGGCCATGCCGCTGCAC 819
Qy 216 -----AlaGlyPheSerThrThrSerSer 223
Db 820 AGGTATGGGTGGGTGAGCGCGCCCTAGCGCGTGGGCGCGGAGGCACCTCGGGGGT 879
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 880 GCGGTGGGGC-----GGCTCCGTGGCTTCAACCCACCTCCAGCTCCGCGC--- 924
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal 263
Db 925 -----AGCTCCTCAGGGGCACCTGAGAGCCGCGC----- 954
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 955 -----TCACTCAAGAGGGGCTCCAAGCCGTCG 981
Qy 284 SerGluSerAlaAlaLeuArgGlnArg-----GluTyr 294
Db 982 GCGTCTCGGCTCGCTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCAACCAGCGC 1041
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 1042 TTTCGGCTGTCTCGGGACAGGAAGTGGCCAAGTCGCTGGCGGTCACTCGTGGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 1102 GGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGCGCGCTGCATGGCCAC 1161
Qy 335 GluArgProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 1162 TGGTCCCT---GACTACTGTGTAAGAAACCTCCTTCTGGCTCCTGTGGGCCAACTCGGCT 1218
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
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Search completed: May 25, 2006, 01:57:12
Job time : 435 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: May 25, 2006, 13:57:39 ; Search time 1529 Seconds
(without alignments)
4713.341 Million cell updates/sec

Title: US-10-626-445-8
Perfect score: 2048
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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2	2035	99.4	1176	10 US-10-626-126-5	Sequence 5, Appli
3	2035	99.4	1176	10 US-10-626-398-5	Sequence 5, Appli
4	1745	85.2	1176	9 US-10-626-445-6	Sequence 6, Appli
5	1745	85.2	1176	10 US-10-626-126-6	Sequence 6, Appli
6	1745	85.2	1176	10 US-10-626-398-6	Sequence 7, Appli
7	1370.5	66.9	1170	10 US-10-488-421-7	Sequence 1, Appli
8	1370.5	66.9	1173	3 US-09-812-216-1	Sequence 1, Appli
9	1370.5	66.9	1173	3 US-09-910-411-1	Sequence 1, Appli
10	1370.5	66.9	1173	3 US-09-875-076-13	Sequence 13, Appli
11	1370.5	66.9	1173	3 US-09-876-252-13	Sequence 13, Appli
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17	1370.5	66.9	1173	8 US-10-349-253A-1	Sequence 1, Appli
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34	1366.5	66.7	1265	10 US-10-488-421-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5
Alignment Scores: 1.91e-214 Length: 1176
Pred. No.: 1

Score: 2035.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.4% Indels: 0
DB: 9 Gaps: 0

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Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGGCACAGCTGCTCAGGTCCCTTGGCATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGCTCTCAATTTGGCTTTGTATTAATGGTAGCAATGCTGGTCACTTTAGCCCTT 120

Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
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Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATTTGGTGTGTTGG 420

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Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
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Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
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RESULT 2

US-10-626-126-5

; Sequence 5, Application US/10626126

; Publication No. US20050074770A1

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Liu, Changlu

; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

; FILE REFERENCE: PRD-0033

; CURRENT APPLICATION NUMBER: US/10/626,126

; CURRENT FILING DATE: 2003-07-23

; PRIOR FILING DATE: 2001-02-22

; PRIOR FILING DATE: 2000-05-31

; PRIOR FILING DATE: 2000-05-31

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5

; LENGTH: 1176

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-626-126-5

Alignment Scores:

Pred. No.: 1,91e-214 Length: 1176

Score: 2035.00 Matches: 390

Percent Similarity: 99.7% Conservative: 0

Best Local Similarity: 99.7% Mismatches: 1

Query Match: 99.4% Indels: 0

DB: 10 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-126-5 (1-1176)

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Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGGCACAGCTGCTCAGGTCCCTTGGCATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaMetValGlyAsnAlaValIleLeuAlaPhe 40

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Db 1081 CCVTTGTGTACAGCGCTTTCCAGAGGCTTTCTGGAAGATACATTTGTGTGACAAAGCAA 1140
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Db 1141 CCAGCGCTGTCCAGAACCAAGTCAATCTCTCT 1173
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RESULT 3

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US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
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; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5
Alignment Scores:
Pred. No.: 1,91e-214 Length: 1176
Score: 2035.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.4% Indels: 0
DB: 10 Gaps: 0
US-10-626-445-8 (1-391) x US-10-626-398-5 (1-1176)
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCAATT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGTCTTCAATTGGCTTTGCTTATAATGGTAGGCAATGCTGTGTCATCTTAGCCTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTTCCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTCTGGGGTTGATTTCATTCCTCTGTACATCCCTCAGGTGTTGTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
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Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTCCTGGCTTCAGATTCTTGGAGAACAGC 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
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Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 541 ATGCTCTTGGATTCCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600
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Db 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGGCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCTCTTCCAGTGTCTCAGGACACTTACACAGAGCTGGGGTGGCTTCGAGGACAAAGTAAT 720
Qy 241 ProGlyLeuLysGluSerAlaSerArgHisSerGluSerProArgArgLysSerSer 260
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Qy      321  TyrCysLeuPheThrIleValLeuSerThrTyProArgThrGluArgProLysSerVal 340
Db      961  TACTGTCTGTTCAAAATGTCCTTCACTTACCCAGAGCGGAAACGCCCCCAATCGGTG 1020
Qy      341  TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db      1021  TGGTACAGCATTGGCTTCGGCTGCAATGGTTCAAATTCGTTTGTAAATCCCTTCTGTAC 1080
Qy      361  ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1081  CCTTTGTGTACAGCGCTTTCAGAGCGCTTTCGGAAGGATCTTTGTGTGACAAAGCAA 1140
Qy      381  ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db      1141  CCAGCGCTGTACAGAACCAAGTCAAGTATCTTCT 1173

RESULT 4
US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Alignment Scores:
Pred. No.:      2,73e-182      Length:      1176
Score:          1745.00      Matches:      332
Percent Similarity: 89.3%      Conservative: 17
Best Local Similarity: 84.9%      Mismatches:  42
Query Match:      85.2%      Indels:       0
DB:               9          Gaps:          0

US-10-626-445-8 (1-391) x US-10-626-445-6 (1-1176)

Qy      1  MetSerGluSerAsnSerThrGlyIleLeuProProAlaIleGlnValProLeuAlaPhe 20
Db      1  ATGTCGAGAGTCTAAACGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
Qy      21  LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db      61  TTAATGTCCTGCTGCTTTGTGTATACGATAGGCAATGCTGGTCAATTTAGCCTTT 120
Qy      41  ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db      121  GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTAATTTTCTTAATTTGGCTATTCT 180
Qy      61  AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db      181  GACTTCTTCGGGTGTCATCTCCATCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
Qy      81  AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
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Db      241  AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTACTCATATCTTTTGTGACACAGA 300
Qy      101  SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db      301  TCGTCTACAGTATTTGTCCTCATTTAGCTACGATCGATACCAAGTCAGTTTCAAAGCGTTG 360
Qy      121  SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db      361  CGTTATAGACACAGACACATGGCATCTGAAATTTGTTCTCAAAATGGTGGCTGTTTGG 420
Qy      141  IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db      421  ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGAATTCCTTGGAAAGACG 480
Qy      161  ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db      481  ACCAACACAGAGAGAGTGGAGCTTGGCTTTGTTACTGAGTGGTACATCTTCGCCATTACA 540
Qy      181  MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db      541  GCATTCTTGGAAATTCCTGCTCCCTGCTCTCTGGTGTCTATTTTCAGTGTACAGATTAC 600
Qy      201  TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db      601  TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCTAGCCACGCTGGATTCTATCGCT 660
Qy      221  ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db      661  ACCTCTTCCAGGGCACTGGACACTCAGCAGAACTGGGTGGCTTTAGGACAAAGTCTT 720
Qy      241  ProGlyLeuLysGluSerAlaLeuSerArgHisSerGluSerProArgArgLysSerSer 260
Db      721  CCTGGATTAAAGGAACCCAGCCGATCCTTCATTTCAGAAAGTCCACGAGGAAGACGAGT 780
Qy      261  IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db      781  CTCCTGGTGTCTTAAGGACTCATGAGCGGTAGTATCATCGCTTCCTCAAGTGGGTTC 840
Qy      281  PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db      841  TTCGCCGATCAGAAAGCCAGTCTTCACAGAGAGAGACGCTGGAGCTTCTCAGAGGC 900
Qy      301  ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db      901  AGGAAGTACGCCAGGTGCTGCTAGTCTCTCTGAGTGTCTTGGCAATTTGCTGGGCTCCG 960
Qy      321  TyrCysLeuPheThrIleValLeuSerThrTyProArgThrGluArgProLysSerVal 340
Db      961  TATTGGCTGTTCACAATTTGTTCTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT 1020
Qy      341  TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db      1021  TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCATTTCAATTCATTATTAATCCCTTCTATAC 1080
Qy      361  ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1081  CCTTTGTGCCACAGACGCTTTCAGAGAGCTTTCGGAAGATACATCTGTGTGACAAAGCAA 1140
Qy      381  ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db      1141  CCAGACCTTTCACAGACCCAGTCAAGTATCTTCT 1173

RESULT 5
US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
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; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Alignment Scores:

Pred. No.: 2,73e-182 Length: 1176
Score: 1745.00 Matches: 332
Percent Similarity: 89.3% Conservatives: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 10 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-126-6 (1-1176)

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Qy 1 MetSerGluSerAenSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAAACGCACTGAGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATT 60

Qy 21 LeuMetSerPheAlaPheAlaIleMetValGlyAenAlaValAlaPhe 40
Db 61 TTAATGCTCCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGGTCAATTTAGCCTTT 120

Qy 41 ValValAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenAlaIleSer 60
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180

Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTCTGGGTGTCATCTCACTCTCTGTACATCCCTCACAGCTGTTTAACTGG 240

Qy 81 AspPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaVal 120
Db 301 TCCGCTACAGTATTGTCTCATTAGTACGATCGATCAGTCAAGTCAAGTCAAGTCAAG 360

Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 CGTTATAGACACAGCACACTGGCATCTGNAATTTGTTGCTCAATGGTGGCTTTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAenSer 160
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGATTCTTGGAGAACAGC 480

Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrIleLeuThrIleThr 180
Db 481 ACCAACACAGAGGAGTGGAGCTTGTGTTACTGAGTGGTACATCTCGCCATTACA 540

Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAenValGlnIleTyr 200
Db 541 GCATCTTGGAAATTCCTGCTCCCTGCTCTCTCTGGTGGTCTATTTCAGTACAGATTAC 600

Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGGAGCTGTGGAGCGTGGAGTCTCAGTAGGTGGCTTAGCCACGCTGGATTCTATCGCT 660

Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTGGCTTGTAGCACAAGTCTT 720

Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
Db 721 CCTGGATTAAAGGAACCCAGCGCATCCCTCATTTTCAAGAAAGTCCACGAGGAAGAGCAGT 780
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Qy 261 IleLeuValSerLeuArgThrHisMetAenSerSerIleThrAlaPheLysValGlySer 280
Db 781 CTCCTGGTGTCTTAAAGGACTCATGAGCGGTAGTATCATCGCCTTCAAGTGGGTTC 840

Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 841 TTTGCGCATCAGAAAGCCAGTCTTCCACGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900

Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCAGTCTGCTGCTCTGAGTCTTTCCTGAGTCTTTTGCATTTGCTGGCTCCG 960

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 961 TATTGGCTGTTCACATTTGTTTCAACTTATTCGACAGAGGGAGCGCCCAAAATCGATT 1020

Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTTCACTTATTATCCCTTCTATAC 1080

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1081 CCTTTGTGCACAGACGTTTCCAGAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140

Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1141 CCAGCACCTTCCACAGACCCAGTCAGTATCTTCT 1173
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RESULT 6

US-10-626-398-6

; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6

Alignment Scores:

Pred. No.: 2,73e-182 Length: 1176
Score: 1745.00 Matches: 332
Percent Similarity: 89.3% Conservatives: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 10 Gaps: 0

US-10-626-445-8 (1-391) x US-10-626-398-6 (1-1176)

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Qy 1 MetSerGluSerAenSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAAACGCACTGAGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATT 60

Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAenAlaValAlaIleLeuAlaPhe 40
Db 61 TTAATGCTCCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGGTCAATTTAGCCTTT 120

Qy 41 ValValAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeuAlaIleSer 60
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTCT 180
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Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTCGTGGTGATCACTCCATCTCTGTACATCTCCCTACACGCTGTTTAACTGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCACTACTGACTATCTTTTGTGCACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCGCTGTACAGTATTGTCTCACTAGCTAGCATCGATACCACTGAGTTCAGTTTCAAAAGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAATGGTGGCTGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGATCTTGGAGAACAGC 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTrpIleLeuThrIleThr 180
Db 481 ACCAACACAGAGAGTGCAGCTGGCTTGTCTACTGAGTGGTACATCTCGCCATTACA 540
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 541 GCATCTTGGAAATCTCTGCTCCCTGCTCTCTGGTGGTCTATTTTCAGTGATACAGATTTC 600
Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 601 TGGAGCTGTGGAGCTGGGAGTCTCAGTAGTGCCCTAGACACGCTGGATTATCATGCT 660
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 661 ACCTCTTCCAGGGCACATGGACACTACGACAGAACTGGTGGTCTGTAGGACAAAGTCTT 720
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSer 260
Db 721 CCTGGATTAAAGGAACACAGCCGATCCCTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 781 CTCCTGTGTCTTAAAGACTCACATGACGGTAGTATCATCGCTTCAAAAGTGGTTC 840
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 841 TTCTGCCGATCAGAAAGCCAGTGTCTTCCACGAGAGACGCTGGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGTGCCTGCTCTCTGAGTCTTGTGCAATTTGCTGGGCTCCG 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 961 TATTGCTGTTCACAATGTCTTTCACATATATCGACAGGGAGCGCCCAATCGATT 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTAATTCACCTTATTAATCCCTTCTATAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1081 CCTTTGTGCCACACAGCTTTCAGAGGCTTCTGGAAGACTCTCTGTGTGACAAAGCAA 1140
Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1141 CCAGCACCTTCACAGACCCAGTCACTATCTCT 1173
RESULT 7
US-10-488-421-7
; Sequence 7, Application US/10488421
; Publication No. US20050239065A1
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GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc. [US/US]
; APPLICANT: Gallagher, Michael J.
; APPLICANT: Yates, Stephen L.
; TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES
; FILE REFERENCE: 1367-13335W001
; CURRENT APPLICATION NUMBER: US/10/488,421
; CURRENT FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US 60/316,762
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/332,697
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent
; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu et al., Mol.
; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequen
; OTHER INFORMATION: are AAG and 988 is C
US-10-488-421-7

Alignment Scores:
Pred. No.: 9,02e-141 Length: 1170
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best Local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 10 Gaps: 2

US-10-626-445-8 (1-391) x US-10-488-421-7 (1-1170)

Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Db 1 ATGCAGATCTATATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAACACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTCGTGGTGATCTCCATTCCTTTGTAGATCCCTCCTACACGCTGTTTCAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100


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Db 241 GATTTTGAAGGAAGAACTGGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTTGCTCATCAGCTATGATGATACCTGTGAGTCTCAAAATGCTGTG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATCTAGGCGTCTGAAGATTTGTTACTCTGATGGTGGCGGTTTG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGCCCAATGATTTAGTTTCAGAGTCTTGGAGAGTAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATACCTCTGCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGATCCCATCTAGTCTAGTCTTATTTTCAACATGAATATTTAT 594
Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 595 TGGAGCCTGTGGAAGCGTATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 655 GTCTCTTCCAACATCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCTCTGCATCTCTTCAATTCAGAGACACAGAGAGAGAGTAGT 774
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTTCAAGAACCAAGATAGCAATACAAATGCTTCCAAATGGGTTC 834
Qy 281 PheTyrSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCAAAGGGAACATGTTGAAGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTyrAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATTTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
Db 955 TATTTCTCTGTTCACAAATGTCTTCAATTTATTTCTCAGCAACAGGTCTCAAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTyrPheLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGATTTGCAATTTGGCTTCAAGTGTTCATTTCTTGTTCATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgPheGlnLysAlaPheTyrLysIleLeuCysValThrLysTyr 380
Db 1075 CCATTTGTGTCAACAGCGCTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln-----AsnGlnSerValSerSer 391
Db 1135 CCTCTACCATCACAAACAGTCGGTCAATCTCTCT 1170
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RESULT 8
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.

```

; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/812,216  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/414,010  
; PRIOR FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-812-216-1  
Alignment Scores:  
Pred. No.: 9,05e-141 Length: 1173  
Score: 1370.50 Matches: 267  
Percent Similarity: 78.3% Conservative: 40  
Best Local Similarity: 68.1% Mismatches: 82  
Query Match: 66.9% Indels: 3  
DB: 2 Gaps: 2  
US-10-626-445-8 (1-391) x US-09-812-216-1 (1-1173)  
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20  
Db 1 ATGCACATACTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40  
Db 61 TTTATGTCTTCTAGTAGCTTTTGTCTATATGCTTAGGAAATGCTTTGGTCATTTTAGCTTTT 120  
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTATTTTTTCTTAATCTGGCCATCTCT 180  
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80  
Db 181 GACTTCTTTGGGTGTGATCTCCATCTCTTTGTATCCTCCCTCACAGCTGTTCCGATGG 240  
Qy 81 AsnPheGlySerGlyIleCysMetPheTyrIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 GATTTTGAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
Db 301 TCTGTATATACATTTGCTCATCAGCTATGATGATACCTGTGAGTCTCAAAATGCTGTG 360  
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140  
Db 361 TCTTATAGAACTCAACATCTAGGCGTCTTGAAGATTTGTTACTCTGATGGTGGCGGTTTG 420  
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160  
Db 421 GTGCTGGCCCTTCTTAGTGAATGGCCCAATGATTTCTAGTCTTCTGAGAGTCTTGGAGAGTAA 480  
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180  
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATACCTCTGCCATCACA 534  
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  
Db 535 TCATTTCTTGGAAATTCGATCCCATCTAGTCTAGTCTTATTTTCAACATGAATATTTAT 594  
Qy 201 TrpSerLeuTyrLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220  
Db 595 TGGAGCCTGTGGAAGCGTATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654  
Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240  
Db 655 GTCTCTTCCAACATCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714
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QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
 Db 715 TCTGCATCGCAGAGAAGTCTCTGATCTCTTCAATTCAGAGAGACAGAGAGAAAGATAGT 774
 QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
 Db 775 CTCAATGTTTCTCACAAGAACCAAGATGAATAGCAATACAAATTCCTCCAAAATGGGTTC 834
 QY 281 PheTrpArgSerGluSerAlaAlaLeuArgGluThrAlaGluLeuLeuArgGly 300
 Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTGAACCTGTAGAGCC 894
 QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
 Db 895 AGAGATTATCCCAAGTCACCTGGCCATCTCTTAGGGGTTTTCTGTGCTGTCTGGCTCCA 954
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 955 TATTCCTGTTCACAAATGTCCTTCAATTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
 Db 1015 TGGTATAGAATTGCATTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTGTAT 1074
 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
 Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGCGCTTCTTGAATAATATTTGTATATAAAGCAA 1134
 QY 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
 Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170

RESULT 9

US-09-910-411-1
 ; Sequence 1, Application US/09910411
 ; Patent No. US20020137054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bergsma, Derk
 ; APPLICANT: Fitzgerald, Laura
 ; APPLICANT: Li, Xiatong
 ; APPLICANT: Michalovich, David
 ; APPLICANT: Zhu, Yuan
 ; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
 ; FILE REFERENCE: GP70655-2C1
 ; CURRENT APPLICATION NUMBER: US/09/910,411
 ; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 09/693,761
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/497,790
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/431,898
 ; PRIOR FILING DATE: 1999-11-02
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-910-411-1

Alignment Scores:

Pred. No.: 9,05e-141 Length: 1173
 Score: 1370.50 Matches: 267
 Percent Similarity: 78.3% Conservative: 40
 Best Local Similarity: 68.1% Mismatches: 82
 Query Match: 66.9% Indels: 3
 DB: 3 Gaps: 2

US-10-626-445-8 (1-391) x US-09-910-411-1 (1-1173)

QY 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
 Db ||| :|||:||||| ||| :||| :||| :|||:|||||

Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCATCAAGCACCTCGTGTACTTTAGCATTT 60
 QY 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
 Db 61 TTTATGTCTTGTAGTAGTCTTGTATTAAGTCTAGGAATGCTTTGTCTCATTTTAGCTTTT 120
 QY 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
 Db 121 GTGTGTCGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 180
 QY 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
 Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACCTCCCTCACACGCTGTTCGAATGG 240
 QY 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuLeuCysThrAla 100
 Db 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCCTACTACTGACTATCTGTATATGTACAGCA 300
 QY 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
 Db 301 TCTGTATATAACATTCCTCATCAGCTATGATCGATACCTGTCACTCTCAAAATGCTGTG 360
 QY 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
 Db 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCGGTGTG 420
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
 Db 421 GTGCTGCCCTTCTTAGTGAATGGGCCAATGATTCCTAGTTTCAGAGCTTGGAGAGATGAA 480
 QY 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
 Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTTGCATCACA 534
 QY 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
 Db 535 TCATTCTTGGAAATTCGTGATCCCAAGTCATCTTAGTCGCTTATTTTCAACATGAATATTTAT 594
 QY 201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
 Db 595 TGGAGCTGTGGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGACGACTGCTGCT 654
 QY 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
 Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGAGATCTCTT 714
 QY 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
 Db 715 TCTGCATCGACAGAAGTCTCTGCATCCTTTTCATTCAGAGAGACAGAGAGAAAGATAGT 774
 QY 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
 Db 775 CTCAATGTTTCTCACAAGAACCAAGATGAATAGCAATACAAATTCCTCCAAAATGGGTTC 834
 QY 281 PheTrpArgSerGluSerAlaAlaLeuArgGluThrAlaGluLeuLeuArgGly 300
 Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTGAACCTGTAGAGCC 894
 QY 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
 Db 895 AGGAGATTAGCCCAAGTCACCTGGCCATTCCTTAGGGGTTTTCTGTGCTGTTCGGGCTCCA 954
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 955 TATTCCTGTTCACAAATGTCCTTTCAATTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
 Db 1015 TGGTATAGAATTGCATTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTGTAT 1074
 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
 Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGCGCTTCTTGAATAATATTTGTATATAAAGCAA 1134

Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
 Db 1135 CCTTACCATCACACACAGTCGTCGTCATCTTCT 1170

RESULT 10
 US-09-875-076-13
 ; Sequence 13, Application US/09875076
 ; Publication No. US20030017528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/09/875,076
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: 09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,439
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,567
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/141,448
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 60/156,653
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,633
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,555
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/156,634
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/157,280
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,294
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,281
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,293
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,282
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-875-076-13

Alignment Scores:
 Pred. No.: 9.05e-141 Length: 1173
 Score: 1370.50 Matches: 267
 Percent Similarity: 78.3% Conservative: 40
 Best Local Similarity: 68.1% Mismatches: 82

Query Match: 56.9% Indels: 3
 DB: 3 Gaps: 2

US-10-626-445-8 (1-391) x US-09-875-076-13 (1-1173)

Qy 1 MetSerGluSerAenSerThrGlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
 Db 1 ATGCCAGATACATAATAGACACATCAATTTATCATAAGCACTCGTGTACTTTAGCATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAenAlaValValIleLeuAlaPhe 40
 Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTAGCTTTT 120

Qy 41 ValValAspArgAenLeuArgHisArgSerAenTyrPhePheLeuAenLeuAlaIleSer 60
 Db 121 GTGGTGGACAAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAAGTGGCCATCTCT 180

Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAenTyr 80
 Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTGCAATGG 240

Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
 Db 241 GATTTTGGAAAGGAATCTGTGTATTGCTGCTCACTACTGACTATCTGTTATGTACAGCA 300

Qy 101 SerValTyrAenIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaVal 120
 Db 301 TCTGTATATAACATTTGCTCCTCATCAGCTATGATCATCCTGTCAGTCTCAAAATGCTGTG 360

Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValIleValAlaGlnMetValAlaValTyr 140
 Db 361 TCTTATAGAACTCAACATATCTGGGGTCTTGAAGATGTTACTCTGTGAGTGGCGCTTTGG 420

Qy 141 IleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAenSerTrpLysAenSer 160
 Db 421 GTGCTGGCCTTCTTAGTGAATGGCCCAATGATCTAGTTTCAGAGTCTTGGAGAGATGAA 480

Qy 161 ThrAenThrLysAspCysGluProGlyPheValThrGluTyrTyrIleLeuThrIleThr 180
 Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534

Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAenValGlnIleTyr 200
 Db 535 TCATTTCTTGGAAATTCGGATCCCATCATCTAGTCGCTTATTTTCAACATGAATATTAT 594

Qy 201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
 Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGTGCCCAAGCCATCCTGGACTGACTGCT 654

Qy 221 ThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAen 240
 Db 655 GTCTCTTCCAAATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
 Db 715 TCTGCATCGACAGAGGTTCTCTGCATCTTTCATTCAGAGACAGAGAGAGAGAGTAGT 774

Qy 261 IleLeuValSerLeuArgThrHisMetAenSerSerIleThrAlaPheLysValGlySer 280
 Db 775 CTCATGTTTTCTTCAGAACCAAGATGATAGCAATACAAATGCTTCCAAAATGGTTC 834

Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
 Db 835 TTCTCCCAATCAGATTCTGTAGTCTTTCACCAAAAGGGAACATGTTGAACCTGCTTAGAGCC 894

Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
 Db 895 AGGAGATTGCCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGCTTTGCTGGGCTCCA 954

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 955 TATTCCTCTGTTCAATTTGTCCTTTTCATTTTATTTATTCCTCAGCAACAGGTCCTTAATCAGTT 1014

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Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTCCTTTGTCATCCCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db 1075 CCATTGTGTACAGCGCTTTCAAAGGCTTCTTGAAGATATTTTGTATAAAAGCAA 1134
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1135 CCTTACCATCAACAACAGTCGTCAGTATCTTCT 1170
RESULT 11
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
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; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-876-252-13
Alignment Scores:
Pred. No.: 9,05e-141 Length: 1173
Score: 1370.50 Matches: 267
Percent Similarity: 78.3% Conservative: 40
Best local Similarity: 68.1% Mismatches: 82
Query Match: 66.9% Indels: 3
DB: 3 Gaps: 2
US-10-626-445-8 (1-391) x US-09-876-252-13 (1-1173)
Qy 1 MetSerGluSerAsnSerThrGlyIleLeuProAlaGlnValProLeuAlaPhe 20
Db 1 ATGCAGATACTAATAGCACAAATCAATTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATATGCTAGAAATGCTTTGGTCATTTTAGCTTTT 120
Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGCAACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTGAAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTATTTTGGCTCACTACTGCTATCTGTTATGTATGTACACA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCATCAGCTATGATGATGATGATGATGATGATGATGATGATG 360
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGGATGAA 480
Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db 481 GGATG-----GAATGTGAACCTGGATTTTTTTTCGGAATGGTACATCCTTCCCATCACA 534
Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGTGATCCCACTCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
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Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
 Db 1135 CCTCTACCATCAACAAACAGTCGGTCAAGTATCTTCT 1170

RESULT 13
 US-10-272-983-13
 ; Sequence 13, Application US/10272983
 ; Publication No. US20030148450A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/10/272,983
 ; CURRENT FILING DATE: 2002-10-17
 ; PRIOR APPLICATION NUMBER: US/09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,439
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,567
 ; PRIOR FILING DATE: 1999-05-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-272-983-13

Alignment Scores:
 Pred. No.: 9.05e-141 Length: 1173
 Score: 1370.50 Matches: 267
 Percent Similarity: 78.3% Conservative: 40
 Best Local Similarity: 68.1% Mismatches: 82
 Query Match: 66.9% Indels: 3
 DB: 7 Gaps: 2

US-10-626-445-8 (1-391) x US-10-272-983-13 (1-1173)

Qy 1 MetSerGluSerAsnSerThrGlyLeuProProAlaAlaGlnValProLeuAlaPhe 20
 Db 1 ATGCCAGATACATAATAGCACAATCAATTTATCACTAAGCACTCGTGTGTTAGCATTT 60

Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40
 Db 61 TTTATGTCCTTAGTACGCTTTTGGCTATATGCTAGGAATGCTTTGGTCATTTTACGCTTT 120

Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
 Db 121 GTGGTGACAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCT 180

Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
 Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCCACAGCTGTTCGAATGG 240

Qy 81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100
 Db 241 GATTTTGGAAAGGAAATCTGTGTTATTTGGCTCACTACTGACTATCTGTATGTACACGA 300

Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
 Db 301 TCTGTATATAACATTTGCTCATCATGATATGATCGATACCTGTCAAGTCTCAATATGCTGTG 360

Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
 Db 361 TCTATAGAACTCAACATCTGGGTCTTGAAGATGTTACTCTGATGGTGGCGGTTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
 Db 421 GTGCTGGCCTTCTTAGTGAATGGCCAAATGATTTCTAGTTTTCAGAGTCTTGGAGAGTAA 480

Qy 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
 Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCATCACA 534

Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
 Db 535 TCATTTCTGGAATTCGATGCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594

Qy 201 TrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
 Db 595 TGGAGCCTGTGGAAGCGTATCATCTCAGTAGGTGCCAAAGCCATCTGGAGTACGCTCT 654

Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
 Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGAGATCTCT 714

Qy 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
 Db 715 TCTGCATCGACAGAAGTTCTCTGATCTTCTTCAATTCAGAGACAGAGAGAGAGTAGT 774

Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
 Db 775 CTCATGTTTCTCCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAAATGGGTTC 834

Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
 Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCACCAAGGGAACATGTTGAACCTGTAGAGCC 894

Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
 Db 895 AGGAGATTAGCCAAAGTCACGTGGCATCTCTTAGGGGTTTTTGTGCTTTGCTGGCTCCA 954

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
 Db 955 TATTCTCTGTTTCACAATTTGCTTTTCAATTTTATTTCTCAGCAACAGGGTCTCTAAATCAGTT 1014

Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
 Db 1015 TGGTATAGAATTCGATTTTGGCTTCAATTCCTTTGCAATTCCTTTGCAATTCCTTTTGTAT 1074

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
 Db 1075 CCATTTGTTCACAGCGCTTTTCAAAAGCCTTTCTTGAANAATATTTTGTATATAAAGCA 1134

Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
 Db 1135 CCTTACCATCAACACACAGTCGGTCAAGTATCTTCT 1170

RESULT 14
 US-10-354-769-1
 ; Sequence 1, Application US/10354769
 ; Publication No. US20030149242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc.
 ; APPLICANT: O'Reilly, Mark A.
 ; APPLICANT: Peter, Beate
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE


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; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1

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US-10-626-445-8 (1-391) x US-10-354-769-1 (1-1173)

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Qy      21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIleLeuAlaPhe 40
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Db      121 GTGTGGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGGCCATCTCT 180

Qy      61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80
Db      181 GACTTCTTTGGGTGTGATCTCATTCCTTTGTACATCCCTCACGCTGTTCGAATGG 240

Qy      81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
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Qy      101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db      301 TCTGTATATAACATTTGCTCATCAGCTATGATCGATACCTGTGCTCAGTCTCAAAATGCTGTG 360

Qy      121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTrp 140
Db      361 TCTTATAGAACTCAACATCTGCGGTCTTGAAGATTTGTTACTCTGTGTTGGCGCTTTGG 420

Qy      141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
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Qy      161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180
Db      481 GGAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCCATCACA 534

Qy      181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAenValGlnIleTyr 200
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Db      595 TGGAGCTTGGAAAGCGTGTATCTCTCAGTAGGTGCCAAGGCCATCTCTGACTGACTGCT 654
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Qy      241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260
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Qy      261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280
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Qy      281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db      835 TTTCCCAATCAGATTTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTCTTAGAGCC 894

Qy      301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
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Qy      361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
Db      1075 CCATTGTTCTACAAGCGCTTTCAAAAGCTTTCTTGAATATATTTTGTATATAAAGCAA 1134

Qy      381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
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RESULT 15
US-10-393-807-13
; Sequence 13, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Llaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
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Searched: 242596 seqs, 56442199 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPO=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1366.5	66.7	1265	7	US-11-242-505A-25
3	297.5	14.5	1847	6	US-10-511-937-2881
4	296	14.5	1323	7	US-11-302-678-42
5	295	14.5	1984	7	US-11-302-678-40
6	295.5	14.4	1074	7	US-11-302-678-39
7	295.5	14.4	1159	7	US-11-302-678-37
8	236.5	11.5	1212	7	US-11-242-505A-16
9	236.5	11.5	1212	7	US-11-242-505A-17

10	207.5	10.1	1143	7	US-11-302-678-21	Sequence 21, Appl
11	207.5	10.1	1182	7	US-11-302-678-19	Sequence 19, Appl
12	207	10.1	1152	7	US-11-304-129-35	Sequence 35, Appl
13	207	10.1	4052	7	US-11-312-958-5	Sequence 5, Appl
14	206.5	10.1	1105	7	US-11-312-958-23	Sequence 23, Appl
15	206	10.1	1727	7	US-11-312-958-11	Sequence 11, Appl
16	205.5	10.0	1179	7	US-11-304-129-39	Sequence 39, Appl
17	204	10.0	1107	7	US-11-302-678-60	Sequence 60, Appl
18	204	10.0	1670	6	US-10-511-937-449	Sequence 449, App
19	204	10.0	1670	7	US-11-302-678-58	Sequence 58, Appl
20	199.5	9.7	2139	6	US-10-511-937-338	Sequence 338, App
21	197.5	9.6	1186	6	US-10-533-300-2	Sequence 2, Appl
22	197.5	9.6	1239	7	US-11-242-505A-13	Sequence 13, Appl
23	197.5	9.6	1239	7	US-11-242-505A-14	Sequence 14, Appl
24	196.5	9.6	1143	7	US-11-304-129-51	Sequence 51, Appl
25	196.5	9.6	1179	7	US-11-304-129-2	Sequence 2, Appl
26	196.5	9.6	1179	7	US-11-304-129-3	Sequence 3, Appl
27	196.5	9.6	1182	7	US-11-312-958-7	Sequence 7, Appl
28	195.5	9.5	1170	7	US-11-302-678-34	Sequence 34, Appl
29	195.5	9.5	1170	7	US-11-302-678-36	Sequence 36, Appl
30	195	9.5	1266	7	US-11-304-129-46	Sequence 46, Appl
31	190.5	9.3	1080	7	US-11-257-851A-74	Sequence 74, Appl
32	190	9.3	1578	6	US-10-473-173-20	Sequence 20, Appl
33	189.5	9.3	1179	7	US-11-304-129-50	Sequence 50, Appl
34	182.5	8.9	1679	6	US-10-473-173-65	Sequence 65, Appl
35	182.5	8.9	1679	6	US-10-505-928-746	Sequence 746, App
36	182.5	8.9	1679	6	US-10-511-937-428	Sequence 428, App
37	182.5	8.9	1679	6	US-10-511-937-2896	Sequence 2896, Ap
38	182.5	8.9	1679	6	US-10-511-937-2918	Sequence 2918, Ap
39	175	8.5	1281	6	US-10-511-937-632	Sequence 632, App
40	173	8.4	3655	6	US-10-511-937-346	Sequence 346, App
41	172.5	8.4	50000	6	US-10-528-659-2	Sequence 2, Appl
42	165.5	8.1	2810	7	US-11-305-477-2	Sequence 2, Appl
43	164	8.0	891	7	US-11-257-851A-72	Sequence 72, Appl
44	161.5	7.9	3100	7	US-11-145-307A-183	Sequence 183, App
45	160.5	7.8	1750	7	US-11-242-111-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-11-242-505A-26
; Publication 26, Application US/11242505A
; Sequence 26, Application US/11242505A
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, c
; FILE REFERENCE: MP12001-288P1RCP1OMNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1173)
US-11-242-505A-26

Alignment Scores:

Pred. No.: 3,49e-120 Length: 1173
Score: 1366.50 Matches: 266
Percent Similarity: 78.1% Conservative: 40
Best Local Similarity: 67.9% Mismatches: 83
Query Match: 66.7% Indels: 3
DB: 7 Gaps: 2

US-10-626-445-8 (1-391) x US-11-242-505A-26 (1-1173)

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Qy 41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTCGAATGG 240
Qy 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrIleLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATCTAGGCGTCTTGAAGATTCTTACTCTGATGGTGGTGGTGG 420
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Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTTAGAGCC 894
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; Sequence 25, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310
; FILE REFERENCE: MPI2001-288P1RCP10NMIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1265
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-242-505A-25
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Alignment Scores:
Pred. No.: 3,9e-120 Length: 1265
Score: 1366.50 Matches: 266
Percent Similarity: 78.1% Conservative: 40
Best Local Similarity: 67.9% Mismatches: 83
Query Match: 66.7% Indels: 3
DB: 7 Gaps: 2

US-10-626-445-8 (1-391) x US-11-242-505A-25 (1-1265)

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Db 175 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAACCTGGCCATCTCT 234
Qy 61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTyr 80
Db 235 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGCTTTCGAATGG 294
Qy 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 81 AsnPheGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100
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Db 295 GATTTTGGAAAGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACGCA 354
Qy 101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 355 TCTGTATATAACATTTGCTCTCATCAGCTATGATGATACCTGTCAGTCTCAATGCTGTG 414
Qy 121 SerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMetValAlaValTyr 140
Db 415 TCTTATAGAATCAACACTACTGGGGTCTTGAAGATTTGTTACTGATGGTGGTCTTGG 474
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrIleAsnSer 160
Db 475 GTGCTGGCTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGCTTGTGAAGATCAA 534
Qy 161 ThrAsnThrIleAspCysGlyProGlyPheValThrGluIleTyrIleLeuThrIleThr 180
Db 535 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATCATCTTGGCCATCACA 588
Qy 181 MetLeuLeuGluPheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
Db 589 TCATTCCTTGGAAATTCGTGATCCCATCTTCTAGTCGCTTATTTCAACATGAATATTAT 648
Qy 201 TrpSerLeuTrpIleAspArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
Db 649 TGGAGCTGTGGAAGCTGTGCTCTCAGTAGGTGCCAAGCCATCTGGACTGCTGCT 708
Qy 221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
Db 709 GTCTCTTCCAACTCTGTGGACACTCATTAGAGGTAGACTATCTTCAAGGAGATCTCTT 768
Qy 241 ProGlyLeuIleGlySerAlaAlaSerArgHisSerGluSerProArgArgIleSerSer 260
Db 769 TCTGCATCGACAGAAGTTCTCGCATCTTCTCATTAGAGAGACGGAGGAGAAAGTAGT 828
Qy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheIleValGlySer 280
Db 829 CTCATGTTTCTCAGAACCAAGATGATGATGATGATGATGATGATGATGATGATGAT 888
Qy 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
Db 889 TTTCTCCCAATCAGATTTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTTAGAGCC 948
Qy 301 ArgIleValAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 949 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTGGGCTCCA 1008
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProIleSerVal 340
Db 1009 TATTCTCTGTTTCAAAATGCTTTCATTTTATTTCTCAGCAACAGGTCTTAAATCAGTT 1068
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 1069 TGGTATAGATTTGATTTTGGCTTCAGTGGTTCAATTCCTTTGTCATCTCTTTTGTAT 1128
Qy 361 ProLeuCysHisArgArgPheGlnIleAlaPheTrpIleValLeuCysValThrIleTrp 380
Db 1129 CCATTGTGTACAAAGCGTTTCAAAAGCGTTTCTTTGAAATATTTTGTATAAAAAAGCAA 1188
Qy 381 ProAlaLeuSerGln---AsnGlnSerValSerSer 391
Db 1189 CCTTACCATCAACAACAGTCGCTGATCTTCT 1224
```

RESULT 3

```
US-10-511-937-2881
; Sequence 2881, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
```

```
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2881
; LENGTH: 1847
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2881
Alignment Scores:
Pred. No.: 5,68e-19 Length: 1847
Score: 297.50 Matches: 100
Percent Similarity: 43.5% Conservative: 62
Best Local Similarity: 26.9% Mismatches: 120
Query Match: 14.5% Indels: 91
DB: 6 Gaps: 14
US-10-626-445-8 (1-391) x US-10-511-937-2881 (1-1847)
Qy 13 AlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGly 32
Db 571 GCATGCAAGATCACCATCCGTCGTCCTTGGCGTCTCTCATCTCATCCATCACCCTTGTGCGC 630
Qy 33 AsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyr 52
Db 631 AATGTGTGCTGTCTGTGGCGTGGGCTTGAACCGCGGCTTCCGCAACCTGACCAATGT 690
Qy 53 PhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeu--- 71
Db 691 TTCATCGTGTCTGTGGCTATCAGTACCTGCTCTCGGCTCTGCTGCTGCTGCTCTCTCT 750
Qy 72 TyrIleProHisValLeuPheAsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeu 91
Db 751 GCCATCTACCAGCTGCTCTGCAAGTGGAGCTTGGCAAGGCTTCTGCAATATCTACACC 810
Qy 92 IleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAsp 111
Db 811 AGCTGTGATGTGATGCTCTGCACAGCTCCATCTTAACCTCTTTCATGATCAGCTCGAC 870
Qy 112 ArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLys 131
Db 871 CGGTACTGCGCTGTCAAGCCACTCGGTGACCTGCTGTGCTGCTGCTGCTGCTGCTGCT 927
Qy 132 IleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIle 151
Db 928 GTGCCCATCTCTCTGCTGCTTAATTTGGTTCATCTCCATACCTGCTCTCTCTCTCTATC 987
Qy 152 LeuAlaSerAspSerTrpLysAsnSerThrAsn-----ThrLysAspCys 166
Db 988 CACCTGGGTGGAAACAGCAGGAAACAGACAGCAAGGCAATCATACCATCTTAAGTGC 1047
Qy 167 GluProGlyPheValThrGluTyrTrpIleLeuThrIleThrMetLeuLeuGluPheLeu 186
Db 1048 AAGTCCAG---GTCAATGAAGTGTACGGGCTG---GTGGATGGGCTGTGTCACCTTCTAC 1101
Qy 187 LeuProValIle-SerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysAr 206
Db 1102 CTCCTGCTACTGATCA----- 1117
Qy 206 gArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerAlaSe 226
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Db 1118 -----TGTGCATCA-----CCTACTACGCATCTTCAAGTC 1149
Qy 226 rGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLysGluSe 246
Db 1150 G-----CCCGGGATCAGG----- 1162
Qy 246 rAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuValSerLeuAr 266
Db 1163 -----CCAAGA----- 1168
Qy 266 gThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArgSerGluSe 286
Db 1169 -----GGATCAATCACATT-----AGTCTCTGGAAG----- 1194
Qy 286 rAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSe 306
Db 1195 -----GCAGCCACCATCAGGAGGACACAAAGCCACAGTGAC 1229
Qy 306 rLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThr-- 325
Db 1230 ACTGGCGCGCTCATGGGGCCCTTCATCATCTGCTGTTCCCTAC-----TTCACCGC 1283
Qy 326 -IleValLeuSerThrTyrProArgThrGluArgProLysSerValTrpTyrSerIleAl 345
Db 1284 GTTTGTGTACCGTGGCTGAGAGGGGATGATGCCATCAATGAGGTGTAGAAGCCATCGT 1343
Qy 345 aPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisAr 365
Db 1344 TCTGTGCTGGCTATGCCAACTCAGCCCTGAAACCCCATCCTGTATCTCGCTGTAACAG 1403
Qy 365 gArgGlnLysAlaPheTrpLysIleLeuCys 376
Db 1404 AGACTTCCGACCGGGTACCACAGCTCTCTGC 1437

RESULT 4
US-11-302-678-42
; Sequence 42, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 4656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PLRNM.OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 1323
```

```
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1323)
; US-11-302-678-42

Alignment Scores:
Pred. No.: 4,8e-19 Length: 1323
Score: 296.00 Matches: 103
Percent Similarity: 41.1% Conservative: 65
Best Local Similarity: 25.2% Mismatches: 136
Query Match: 14.5% Indels: 105
DB: 7 Gaps: 12

US-10-626-445-8 (1-391) x US-11-302-678-42 (1-1323)

Qy 4 SerAsnSerThr-----GlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 25 GCCAATAGCACCCCGCGCTGGGGGCGAGGCGCGCGTGGCGCGCGGCGGCGGCGTGG 84
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetVal-----GlyAsnAlaValValIle 37
Db 85 GTGGCGCGCGCGTGTGCGTGTGTCATCGCGCTGACGGCGCGCGCCAACTCGTCTGCTATC 144
Qy 38 LeuAlaPheValValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 145 GCGCTCATCTGCATCAGCCCGCGCTGGCAACACACAGTCCAACTTCTTCTGTTGTTGCTC 204
Qy 58 AlaIleSerAspPheLeuValGlyIleSerIleProLeuTyrIleProHisValLeu 77
Db 205 TTCAGTCTCACCTGATGTGGGCTGTGGTGTGATGCGCGCGCGCATGCTGAACGCGCTG 264
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 265 TACGGCGCGTGGTGTGGCGCGCGCTCTGCTCTGTCGACCGCGCTTCGACGTGTG 324
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 325 TGTGTGAGCGCTCCATCTCACTCTGCTCATCAGCTTGGACCGCTACCTGCTCATC 384
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMet 136
Db 385 CTCTCGCGCTGCGCTACAAAGTGGCATGACGCGCC---CTGGGTGCGCTGCGCTAGT 441
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGly---ProMetIleLeu-AlaSerAs 155
Db 442 CTGGCGCGCTGGAGCCTCGCGCTCTGCTTCTTCTGCGCGCTGCTGCGGTGGCGAC 501
Qy 155 pSerTrpLysAsn-----SerThrAsnThrLysAspCysGluProGlyPheVa 171
Db 502 GAGTGGGCGACGACGCGCCACCGTCCCTGGCCAGTGGCGCTGTCGGCAGCGCTGCT 561
Qy 171 lThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSe 191
Db 562 TTTTG----- 565
Qy 191 rValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAlaLeuSerAr 211
Db 566 -----TCTTGTGGCGTGGGCGCTCACCTTCTTC 594
Qy 211 gCysProSerHisAlaGlyPheSerThrThrSerSerSer-AlaSer----- 226
Db 595 CTGCCCTCGGGTGCCATATGCTTCACCTACTGACAGGATCTCTGTAGTGGCCGCAAGCAG 654
Qy 227 -----GlyHisLeuHisArg-AlaGlyValAlaCys----- 236
Db 655 GCGGTGAGGTGGCTCCCTCACCGGCATGGCCAGTCAAGGCTCGGAGACGCTGCAG 714
Qy 237 -----ArgThrSerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSer 254
Db 715 GTGCCCCAGGACCCACCGCGGGGTG---GAGTCTGCTGACACGACGCGCTTACGCCACG 771
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Qy 255 ProHArgLysSerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThr 274
Db 772 AAGCACAGCAGGAAGCCTGAAGCCAGCAGCCTG----- 804
Qy 275 AlaPheLysValGlySerPheTrpArgSerAlaAlaLeuArgGlnArgGluTyr 294
Db 804 ----- 804
Qy 295 AlaGluLeuLeuArgGlyArgLysLeuAlaAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db 805 -----ACGCTGGGCATCTCTGGGCATGTC 831
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db 832 TTTGTGACCTGGTGGCTCTTTGTGGCCAAACATAGTCCAGGCCGTG-----TGC 882
Qy 335 GluArgProLysSerValTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
Db 883 GACTGCATCTCCCGAGCCCTTCGATGTCTCATATGGCTGGGTACTGTAAACAGCACC 942
Qy 355 ValAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 943 ATGAACCCCATCTACTACCCACTCTTCATCGGGGACTTCAAGCGGGCGCTGGGCAGGTTT 1002
Qy 375 LeuCysValThrLysTrpPro 381
Db 1003 CTGCCATGTCCACGCTGTCCC 1023

RESULT 5
US-11-302-678-40
; Sequence 40, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (468) ... (1790)
; US-11-302-678-40
```

```
Alignment Scores:
Pred. No.: 8,75e-19 Length: 1984
Score: 296.00 Matches: 103
Percent Similarity: 41.1% Conservative: 65
Best Local Similarity: 25.2% Mismatches: 136
Query Match: 14.5% Indels: 105
DB: 7 Gaps: 12
```

```
US-10-626-445-8 (1-391) x US-11-302-678-40 (1-1984)

Qy 4 SerAsnSerThr-----GlyIleLeuProAlaAlaGlnValProLeuAlaPhe 20
Db 492 GCCAATAGCACCCCGCGCTGGGGGCGAGGGCCGCGCTGGCCCGCGGGGGGCGAGCGGCTGG 551
Qy 21 LeuMetSerSerPheAlaPheAlaIleMetVal-----GlyAsnAlaValIle 37
Db 552 GTGGCGCGCGCTGTGCGTGGTTCATCGCGTGCAGCGCGCGCGGCGCAACTCGCTGCTGATC 611
Qy 38 LeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 612 GCGTCTCATCTGCACCTCAGCCCGCGCTGCGCAACACAGTCCAACCTTCTTCTGCTGCTGCTC 671
Qy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77
Db 672 TTCACGCTCTGACCTGATGGTGGGGCTGGTGTATGCCGCGCCATGCTGAACGCGCTG 731
Qy 78 Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 732 TAGCGGCGCTGGGTGGTGGCGCGCGCTGTGCTGTCTGGACCGCTTCAGTGTATG 791
Qy 97 LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 792 TGTGTCAGCGCTCCATCTCAACCTCTGCTCATCAGCTGGACCGCTACTGCTGCTCATC 851
Qy 117 SerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetIleValAlaGlnMet 136
Db 852 CTCTCGCGCTGGCTGACAGCTGCAGTGCAGCGCC---CTGCGTGGCGCTGGCGCTAGTC 908
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGly---ProMetIleLeu-AlaSerAs 155
Db 909 CTGGCGCGCTGGAGCTCGCGCTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
Qy 155 pSerTrpLysAsn-----SerThrAsnThrLysAspCysGluProGlyPheVa 171
Db 969 GAGCTGGCGCACGACGCGCCACCGCTCCCTGGCGAGTGCAGCGCTGCTGCGCAGCTGCT 1028
Qy 171 LThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSe 191
Db 1029 TTTG----- 1032
Qy 191 rValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAlaLeuSerAr 211
Db 1033 -----TCTTGTGGCGTGGCGCTCACCTTCTTC 1061
Qy 211 gCysProSerHisAlaGlyPheSerThrThrSerSerSer-AlaSer----- 226
Db 1062 CTGCTCTGGGTGCCATATGCTTTCACCTACTGCAGGATCTCTGCTAGTGTGCGCGCAGCAG 1121
Qy 227 -----GlyHisLeuHisArg-AlaGlyValAlaCys----- 236
Db 1122 GCCGTGCAGTGGCTCCCTCACACCGCATGCGCAGTCCAGGCTCGGAGACGCTGAG 1181
Qy 237 -----ArgThrSerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSer 254
Db 1182 GTGCCAGGACCCACGCGCCAGGGGTG---GAGTCTGCTCAGCAGCGCTGCTAGCAGCAG 1238
Qy 255 ProArgArgLysSerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThr 274
Db 1239 AAGCACAGCAGGAAGCCCTGAAGGCCAGCGCTG----- 1271
Qy 275 AlaPheLysValGlySerPheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyr 294
```

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Db      1271 -----1271
QY      295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db      1272 -----ACGCTGGGCAATCTCTGGGCAATGTTTC 1298
QY      315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
Db      1299 TTGTGTACCTGGTGGCTTCTTTGTGGCCAAACATAGTCCAGGCCGTG-----TGC 1349
QY      335 GluArgProLysSerValTrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerPhe 354
Db      1350 GACTGATCTCCCGAGCCCTCTTCGATGCTCTCACATGGCTGGGTACTGTAAACAGCACC 1409
QY      355 ValAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db      1410 ATGAACCCCATCATCACCACTCTTCATCGGGACTTCAAGCGGGCGCTGGCGCAGGTTTC 1469
QY      375 LeuCysValThrLysTrpPro 381
Db      1470 CTGCCATGTCCAGCTGCTCC 1490

RESULT 6
US-11-302-678-39
; Sequence 39, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MP102-012PIRNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1074)
US-11-302-678-39
Alignment Scores:
Pred. No.: 3,93e-19 Length: 1074
Score: 295.50 Matches: 88
Percent Similarity: 44.1% Conservative: 72
Best Local Similarity: 24.2% Mismatches: 134

```

```

Query Match: 14.4% Indels: 69
DB: 7 Gaps: 14
US-10-626-445-8 (1-391) x US-11-302-678-39 (1-1074)
QY      18 LeuAlaPheLeuMet---SerSerPheAlaPheAlaIleMetValGlyAsnAlaValVal 36
Db      139 CTGGGCTTTCTGGTGGCGCGACGTTTCGCTGGAACCTGCTGGT-----183
QY      37 IleLeuAlaPheValValAspArgAsnLeuArgHisArg---SerAsnTyrPhePheLeu 55
Db      184 ---CTGGGACCATCTCTCGGTGTACGACCTTCCACCGCTGCCGCCACACCTGGTGGCA 240
QY      56 AsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHis 75
Db      241 TCCATGGCGCTCTCGATGTCCTGGTGGCGCGCTGTCATGCGCTGAGCCCTGGTGCAT 300
QY      76 ValLeuPhe-----AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThr 93
Db      301 GAGCTGTCCGGGCGCGCTGGCAGTAGGTGCGAGGCTGTGCCAGCTTTTGGATCGCGTGC 360
QY      94 AspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyr 113
Db      361 GAGTGCTTTGTGTCACGCCACATCTGGAAGCTGACGGCCATAGCCCTGGACCGCTAC 420
QY      114 GlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleVal 133
Db      421 TGGTCCATCAGCGCCACATGGAATACACGCTCCGACCGCCGCAAGTGGTCTCCACGCTC 480
QY      134 AlaGlnMetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeu 152
Db      481 -----ATGATCGCGCTCACCTGGGCACCTTCGCGCTGTCTCTCTGGCCCCGCTGCTT 534
QY      153 AlaSerAspSerTrpLysAsnSerThrAsnThrLysAspCys-----GluPro 168
Db      535 TTTGGCTGGGGAGAGACGTACTCTGAGGGCAGCGAGGAGTCCAGGTAAAGCCGCGAGCT 594
QY      169 GlyPheValThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuPro 188
Db      595 TCCTACGCC-----GTGTTCTCCACCGTAGGCGCTTCTACCTGCGC 636
QY      189 ValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAla 208
Db      637 CTCTGTGTGTGCTCTTC-----GTGTACTGGAAGATCTACAAGGTGCC---681
QY      209 LeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerAlaSerGlyHis 228
Db      681 -----681
QY      229 LeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLysGluSerAlaAla 248
Db      682 -----AAGTTCCGCGTGGGCTCCAGGAGACCAATAGCGTCTCACCCATATCGAAGCT 735
QY      249 SerArgHisSerGluSerProArgArgLysSerSerIleLeuValSerLeuArgThrHis 268
Db      736 GTGGAGGTGAAGGACTCTGCCAAACAGCCAGTGGTGTTC-----ACGGTC 783
QY      269 MetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArgSerGluSerAlaAla 288
Db      784 CGCCACGCCACCTCACCTTCCAGCCAGAGGGGACACGTGGCGGGAGCAG-----834
QY      289 LeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAla 308
Db      835 -----AAGGAGCAGCGGGCGCGCTCATGGTGGGC 864
QY      309 IleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeu 328
Db      865 ATCCTCATTTGGCGTGTTCGTGCTCTGCTGATCCCCCTTCTTCTC---ACCGAGCTCATC 921
QY      329 SerThrTyrProArgThrGluArgProLysSerValTrpTyrSerIleAlaPheTrpLeu 348
Db      922 AGTCCCTCTGCTCTGTGTGACATCCCC---GCCATCTGGAAGCATCTTCTCTGCTGCTT 978

```


Qy 349 GlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisArgPheGln 368
 Db 979 GGCTACTCCAACTCCTCTTTAAACCCCTGAICTATACGGCTTTCAACAAGAACTACAAC 1038
 Qy 369 LysAlaPhe 371
 Db 1039 AGCGCCTTC 1047

RESULT 7

US-11-302-678-37
 ; Sequence 37, Application US/11302678
 ; Publication No. US2006008881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Inmaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012P1RNM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: US 60/414,262
 ; PRIOR FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: US 60/419,986
 ; PRIOR FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US 60/423,809
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: US 60/429,797
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 1159
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (64)...(1137)
 US-11-302-678-37

Alignment Scores:
 Pred. No.: 4,4e-19 Length: 1159
 Score: 295.50 Matches: 88
 Percent Similarity: 44.1% Conservative: 72
 Best Local Similarity: 24.2% Mismatches: 134
 Query Match: 14.4% Indels: 69
 DB: 7 Gaps: 14

US-10-626-445-8 (1-391) x US-11-302-678-37 (1-1159)

Qy 18 LeuAlaPheLeuMet---SerSerPheAlaPheAlaIleMetValGlyAsnAlaValVal 36
 Db 202 CTGGGCTTTCTGGGGGCGGACGCTTCGCTGGAACTCTGCTGGTG----- 246
 Qy 37 IleLeuAlaPheValValAspArgAsnLeuArgHisArg---SerAsnTyrPhePheLeu 55
 Db 247 ---CTGGCGACCATCTCTCCGTGTACGACCTTCACCGCGCTGCCCAACACCTGGTGCA 303
 Qy 56 AsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHis 75

Db 304 TCCATGCGCGTCTCGGATGTCCTGGTGGCGCGGTGGTGCATGCGCGTGAGCTGGTGCAT 363
 Qy 76 ValLeuPhe-----AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThr 93
 Db 364 GAGCTGTCCGGGCGCGCTGGCAGCTAGTGGAGGCTGTGCCAGCTTTGGATCGCGTCG 423
 Qy 94 AspTyrIleLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyr 113
 Db 424 GACGTGCTTTGCTGCACGCGCAGCATCTGGAACCATCTGGCCCATAGCGCTCGACGCTAC 483
 Qy 114 GlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleVal 133
 Db 484 TGTTCATACGCGCCACATGGAATACAGCTCCGCACCCCAAGTGGGTCTCCACAGTC 543
 Qy 134 AlaGlnMetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeu 152
 Db 544 -----ATGATCGGCTCACCTGGGCACTCTCCGCTGTGCATCTCTGCGCCCGCTGCTT 597
 Qy 153 AlaserAspSerTrpLysAsnSerThrAsnThrLysAspCys-----GluPro 168
 Db 598 TTTGGCTGGGGAGAGACGTACTCTGAGGCGAGCGAGGAGTGCAGGTAAGCGCGAGCT 657
 Qy 169 GlyPheValThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuPro 188
 Db 658 TCCTACGCC-----GTGTTCTCCACCGTAGGCGCTTCTACTCGCG 699
 Qy 189 ValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrpLysArgAla 208
 Db 700 CTCGTGTGGTGTCTTC-----GTGTACTGGAAGATCTACAAGCTGCC--- 744
 Qy 209 LeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerSerAlaSerGlyHis 228
 Db 744 ----- 744
 Qy 229 LeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLysGluSerAlaAla 248
 Db 745 -----AAGTTCCGCGTGGGCTCCAGGAAGCAACATAGCGTCTCACCCTATCCGAAGCT 798
 Qy 249 SerArgHisSerGluSerProArgArgLysSerSerIleLeuValSerLeuArgThrHis 268
 Db 799 GTGGAGGTGAAGGACCTTGCCAAACAGCCACCCAGATGGTGTTC-----ACGTC 846
 Qy 269 MetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArgSerGluSerAlaAla 288
 Db 847 CGCACGCCACCGTCACCTTCCAGCCAGAAAGGGACACGTCGGCGGAGCAG----- 897
 Qy 289 LeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAla 308
 Db 898 -----AAGGAGCAGCGCGCGCCCTCATGCTGGGC 927
 Qy 309 IleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeu 328
 Db 928 ATCTCATTCGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
 Qy 329 SerThrTyrProArgThrGluArgProLysSerValTrpTyrSerIleAlaPheTrpLeu 348
 Db 985 AGTCCCTCTGCTCTGTGTGACATCCCC---GCCATCTGGAAGAAAGCATCTTCTGTGGCTT 1041
 Qy 349 GlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisArgArgPheGln 368
 Db 1042 GGCTACTCCAACTCCTCTTTAAACCCCTGATCTATACGGCTTTCAACAAGAACTACAAC 1101
 Qy 369 LysAlaPhe 371
 Db 1102 AGCGCCTTC 1110

RESULT 8

US-11-242-505A-16
 ; Sequence 16, Application US/11242505A
 ; Publication No. US2006009656A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carroll, Joseph M.

[illegible]

; LOCATION: (1)... (1212)
US-11-242-505A-17

Alignment Scores:

Pred. No.:	1.75e-13	Length:	1212
Score:	236.50	Matches:	89
Percent Similarity:	36.3%	Conservative:	62
Best Local Similarity:	21.4%	Mismatches:	114
Query Match:	11.5%	Indels:	151
DB:	7	Gaps:	14

US-10-626-445-8 (1-391) X US-11-242-505A-17 (1-1212)

10	LeuProProAlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPheAla	29
112	ATGCCCATCTGTGGCCACATACCTCGTGCATCTTCGTGGCGCT	156
30	MetValGlyAsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArgHisArg	49
157	---GTGGGCAATGGGCTCACCCTGTGTGTCACTCTGGCCACCAAGAGCCATGCGCACGCGCT	213
50	SerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIle	69
214	ACCACTACTACCTCTTCAAGCTGGCCGTGTGCAGCCTGTGTGTGTGTGTGGGCGCTG	273
70	ProLeuTyrIleProHisValLeuPheAsnTrpAsnPhe	87
274	CCCTGGAGCTATAGATGTGGCACAACTACCCCTTCCTGTCTGGCGGTGTGTGGCTGC	333
88	MetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeu	107
334	TATTTCCGACGCTACTCTTTGAGATGCTGTGCCTGGCCTCAGTGTCTCAACGTCACGTGC	393
108	IleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThr	127
394	CTGAGCGTGAACGCTATGTGCCGTGTGCACCCACTCCAGCCAGGTCCATGTGTGAGC	453
128	---GlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeu	145
454	CGGGCCCATGTGGCCGAGTCTGGG	504
146	ValAsn	148
505	TGCTCCCTGCCCAACACCAAGCTGTGCAGGCATCCGGCAGCTGCACGTGCCCTCCCGGGC	564
149	Pro	161
565	CCAGTGCAGACTCAGCTGTTGTGATGCTGTGTCCGCCACCGCGCTCTACAAAC	618
162	AsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThrMet	181
619	-----ATGTAGTGCAGACCACCGCG	639
182	LeuLeuGluPheLeuLeuPro	199
640	CTGCTCTTCTTCGCTCCCATGCCCATCATGAGCTGTCTACCTGTCTCAT	693
200	TyrTrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPheSer	219
693	-----	693
220	ThrThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSer	239
694	-----GGGCTTGGCACTGCGCGCGGAG	714
240	AsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSer	259
715	AGGCTGTGCTCATCGACGAGGCCAAGGGCAGGGGCTCTGCAGCAGCCAGTCCACA	771
260	SerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGly	279
771	-----	771

Qy	280	SerPheTrpArgSerGluSerAlaAlaIleuArgGlnArgGluTyrAlaGluLeuLeuArg	299
Db	772	-----TACCTCGCGGCTCCAGCAGCACGAT-----CGG	801
Qy	300	GlyArgLys---LeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrp	318
Db	802	GGCCGGAGCAAGTGACCAAGATGCTGTTGTCCTGGTCGGTGGTCTTTGGCATCTGCTGG	861
Qy	319	AlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLys	338
Db	862	GCCCGCGTTC-----CACGCCGACCGC	882
Qy	339	SerValTrpTyrSerIleAlaPheTrpLeuGln-----	349
Db	883	GTCATGTGGAGCGTCGTGCACAGTGACACAGATGGCTGCACCTGGCCCTCCAGCACCGTG	942
Qy	350	-----TrpPheAsnSerPheValAsnProPheLeuTyrPro	361
Db	943	CACGTCACTCCGGCATCTTCTTACCTGGGCTCGGGGCCAACCCGCTGCTCTATAGC	1002
Qy	362	LeuCysHisArgArpGlnLysAlaPheTrpLysIleLeuCysVal	377
Db	1003	CTCATGTCAGCGCGCTCCGAGAGACCTTCACAGGAGCGCCCTGTGCCTC	1050
RESULT 10			
US-11-302-678-21			
; Sequence 21, Application US/11302678			
; Publication No. US2006088881A1			
; GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals, Inc.			
; APPLICANT: Silos-Santiago, Immaculada			
; APPLICANT: Venkateswarlu, Karicheti			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING			
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 62553, 302, 323,			
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,			
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOL			
; FILE REFERENCE: MPI02-012PIRNM OMNI			
; CURRENT APPLICATION NUMBER: US/11/302,678			
; CURRENT FILING DATE: 2005-12-14			
; PRIOR APPLICATION NUMBER: US/10/345,680			
; PRIOR FILING DATE: 2003-01-16			
; PRIOR APPLICATION NUMBER: US 60/349,511			
; PRIOR FILING DATE: 2002-01-18			
; PRIOR APPLICATION NUMBER: US 60/360,500			
; PRIOR FILING DATE: 2002-02-28			
; PRIOR APPLICATION NUMBER: US 60/365,041			
; PRIOR FILING DATE: 2002-03-15			
; PRIOR APPLICATION NUMBER: US 60/374,063			
; PRIOR FILING DATE: 2002-04-19			
; PRIOR APPLICATION NUMBER: US 60/403,468			
; PRIOR FILING DATE: 2002-08-14			
; PRIOR APPLICATION NUMBER: US 60/414,262			
; PRIOR FILING DATE: 2002-09-27			
; PRIOR APPLICATION NUMBER: US 60/419,986			
; PRIOR FILING DATE: 2002-10-21			
; PRIOR APPLICATION NUMBER: US 60/423,809			
; PRIOR FILING DATE: 2002-11-05			
; PRIOR APPLICATION NUMBER: US 60/429,797			
; PRIOR FILING DATE: 2002-11-26			
; NUMBER OF SEQ ID NOS: 66			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 21			
; LENGTH: 1143			
; TYPE: DNA			
; ORGANISM: Homo Sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)...(1143)			
US-11-302-678-21			
Alignment Scores:			
Pred. No.: 8,75e-11 Length: 1143			
Score: 207,50 Matches: 85			

Percent Similarity:	39.1%	Conservative:	61
Best Local Similarity:	22.8%	Mismatches:	133
Query Match:	10.1%	Indels:	94
DB:	7	Gaps:	12

US-10-626-445-8 (1-391) x US-11-302-678-21 (1-1143)

Qy	10	LeuProAlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPheAlaLe	29
Db	160	ATCTCCCGGGCCATCCCGGTATCATCATCGCGGTCTACTCGTAGTGTTCGTGTGGGC	219
Qy	30	MetValGlyAsnAlaValAlaLeuAlaPheValValAspArgAsnLeuArgHisArg	49
Db	220	TTGGTGGCACTCGCTGGTCTATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCA	279
Qy	50	SerAsnTyrPhePheLeuAsnLeuAlaLeSerAspPheLeuValGlyLeuLeSerIle	69
Db	280	ACCAACATTTACATATTAACTGGCTTTGGCAGATGCTTTAGTT---ACTACAACCATG	336
Qy	70	ProLeuTyrIleProHisValLeuPheAsn---TrpAsnPheGlySerGlyIleCysMet	88
Db	337	CCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTGGGAGTGTCTGTGCAAG	396
Qy	89	PheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIle	108
Db	397	ATAGTAATTTCCATTGATTACTACAACATGTTCCACGAGCATCTTCACCTTGACCATGATG	456
Qy	109	SerTyrAspArgTyrGlnSerValSerAsn-----AlaValSerTyrArgAlaGln	125
Db	457	AGCTGGAGCCGCTACATTGCGGTGTGCCACCCTGGAAAGGCTTTGGACTTCGCGACACCC	516
Qy	126	HisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeu	145
Db	517	-----TTCAAGGCAAGATCATCAATATCTGCATCTGGCTGCTGTCGTCATCT	564
Qy	146	ValAsn---GlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrLys	164
Db	565	GTTCGCATCTCTGCAATATAGTCTCTGGAGGACCAAAAGTCAGGGAAGACGTTCGATGTCA	624
Qy	165	AspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGlu	184
Db	625	GAGTGCTCTTGCACTTCCAGATGATCACTAC-----	657
Qy	185	PheLeuProValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTrp	204
Db	658	-----TCCTGGTGGACCTCTTCTC-----	675
Qy	205	Lys-ArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerSe	224
Db	676	ATGAAGATCTCGCTCTTTCATCTTCCCTTCGGTGATCC-----	712
Qy	224	rAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu	244
Db	713	-----CTGTC	717
Qy	244	sGluSerAlaAlaSerArg-HisSerGluSerPro-ArgArgLysSerSerIleLeuVal	263
Db	718	CTCATCATCATCTGCTGTACACCTCGATGATCTCGGTCCTCAAGAGCGTCCGGCTCCT	777
Qy	264	SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLeuValGlySerPheTrpArg	283
Db	778	TCT-----GGCTCC-----	786
Qy	284	SerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeu	303
Db	787	-----CGAGAGAAGATCGCAACCTG-----CGTAGGATC	816
Qy	304	AlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeu	323
Db	817	ACCAGACTGGTCTGGTGGTGGGGTTTTTCGTGCTGTCTGGACTCCATTTCACATA	876
Qy	324	PheThrIleValLeu-----SerThrTyrProArgThrGluArgProLysSerVal	340

877	TTCA	TCTG	TGGAGG	CTCTGGG	GAGCAC	CTCCAC	AGCAGCTGCTCTCTCCAGCTAT	936
Db								
341	Trp	Tyr	Ser	Ile	Ala	Phe	Trp	Leu
Qy								
937	TACT	TCTGCAT	CGCC-----	TTAGG	TATATACCA	CAACAGTAGCTGAA	TCTCCATTTCTCTAC	990
Db								
361	Pro	Leu	Cys	His	Arg	G	Arg	Phe
Qy								
991	GCCT	TTCTCTGAT	GAAAC	TTCAACG	GGGTTC	1023		
Db								

RESULT 11

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US-11-302-678-19
: Sequence 19, Application US/11302678
: Publication No. US2006008881A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Silos-Santiago, Immaculada
: APPLICANT: Venkateswarlu, Karicheti
:
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
: TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
: TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
: TITLE OF INVENTION: 12303, 985, 12337, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
: FILE REFERENCE: MPIO2-012PRNM OMNI
:
: CURRENT APPLICATION NUMBER: US/11/302,678
: CURRENT FILING DATE: 2005-12-14
: PRIOR APPLICATION NUMBER: US/10/345,680
: PRIOR FILING DATE: 2003-01-16
: PRIOR APPLICATION NUMBER: US 60/349,511
: PRIOR FILING DATE: 2002-01-18
: PRIOR APPLICATION NUMBER: US 60/360,500
: PRIOR FILING DATE: 2002-02-28
: PRIOR APPLICATION NUMBER: US 60/365,041
: PRIOR FILING DATE: 2002-03-15
: PRIOR APPLICATION NUMBER: US 60/374,063
: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: US 60/403,468
: PRIOR FILING DATE: 2002-08-14
: PRIOR APPLICATION NUMBER: US 60/414,262
: PRIOR FILING DATE: 2002-09-27
: PRIOR APPLICATION NUMBER: US 60/419,986
: PRIOR FILING DATE: 2002-10-21
: PRIOR APPLICATION NUMBER: US 60/423,809
: PRIOR FILING DATE: 2002-11-05
: PRIOR APPLICATION NUMBER: US 60/429,797
: PRIOR FILING DATE: 2002-11-26
:
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: Fast-Seq for Windows Version 4.0

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Alignment Scores:		
Pred. No.:	9.2e-11	Length: 1182
Score:	207.50	Matches: 85
Percent Similarity:	35.1%	Conservative: 61
Best Local Similarity:	22.8%	Mismatches: 133
Query Match:	10.1%	Indels: 94
DR:	7	Gaps: 12
		DR:

US-10-626-445-8 (1-391) x US-11-302-678-19 (1-1182)

[illegible]

```
Qy 50 SerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIle 69
Db 293 ACCAACATTACATATTAACTGGCTTGGCAGATGCTTAGTT--ACTACAAACCATG 349
Qy 70 ProLeuTyrIleProHisValLeuPheAsn--TirPheAsnGlySerGlyIleCysMet 88
Db 350 CCCTTTTCAGAGTACGGTCTACTTGATGATTCCTGGCTTTTGGGATGCTGTGCAAG 409
Qy 89 PheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIle 108
Db 410 ATAGTAATTTCCATTTGATTACTACACATGTTCCACGACATCTTCCCTTGACCATGATG 469
Qy 109 SerTyrAspArgTyrGlnSerValSerAsn-----AlaValSerTyrArgAlaGln 125
Db 470 AGCGTGACCGCTACATTTGGCGTGTGCACCCCGCTGAAGGCTTTGGACTTCCGACACCC 529
Qy 126 HisThrGlyIleMetLysIleValAlaGlnMetValAlaValTyrIleLeuAlaPheLeu 145
Db 530 -----TTGAAGGCAGAAAGATCATCATATATCTGCATCTGGCTGTGCTCATCT 577
Qy 146 ValAsn---GlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrLys 164
Db 578 GTTGGCATCTCTGCAATAGTCTTGGAGGCACCAAGTCAGGAAAGACGTCGATGTCATT 637
Qy 165 AspCysGluProGlyPheValThrGluTyrTrpIleLeuThrIleThrMetLeuGlu 184
Db 638 GAGTGTCTCTTGCGATTTCCCGATGATGACTAC----- 670
Qy 185 PheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeuTyr 204
Db 671 -----TCTGGTGGGACCTTCTC 688
Qy 205 Lys-ArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSerSe 224
Db 689 ATGAAGATCTGCGCTTTCATCTTTGCCTTCTGTGATCC----- 725
Qy 224 rAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLy 244
Db 726 -----CTGTC 730
Qy 244 sGluSerAlaAlaSerArg-HisSerGluSerPro-ArgArgLysSerSerIleLeuVal 263
Db 731 CTATCATCATCTGCTGCTACCTGATGATCTGCTGCTCAGAGCGTCCGGCTCCTT 790
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 791 TCT-----GGCTCC----- 799
Qy 284 SerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeu 303
Db 800 -----CGAGAGAAAGATCGCAACCTG-----CGTAGGATC 829
Qy 304 AlaArgSerLeuAlaIleLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeu 323
Db 830 ACCAGACTGCTGCTGGTGGTGGCGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889
Qy 324 PheThrIleValLeu-----SerThrTyrProArgThrGluArgProLysSerVal 340
Db 890 TTATCTCTGCTGGAGGCTCTGGGAGGACCTCCACAGACAGCTGCTCTCTCCAGCTAT 949
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
Db 950 TACTTCTGTCATCGCC-----TTAGGTATACCAACAGTAGTCCGTGATCCCATCTCTAC 1003
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPhe 371
Db 1004 GCCTTTCTTGATGAAAACCTTCAAGCGGTGTTT 1036
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RESULT 12

US-11-304-129-35

; Sequence 35, Application US/11304129

; Publication No. US20060089915A1

```
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; PRIOR FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 35
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Human
; US-11-304-129-35

Alignment Scores:
Pred. No.: 9,87e-11 Length: 1152
Score: 207.00 Matches: 104
Percent Similarity: 39.7% Conservative: 53
Best Local Similarity: 26.3% Mismatches: 141
Query Match: 10.1% Indels: 99
DB: Gaps: 16
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US-10-626-445-8 (1-391) x US-11-304-129-35 (1-1152)

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Qy 13 AlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGly 32
Db 151 GCAGCCAAAGATCGTCATTGGCATTTGGCATTCGCGAGGCATCATGCTGGTCTCGCGCATCGGT 210
Qy 33 AsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyr 52
Db 211 AACTTTGCTTTATCGCTGCCCTCACCCGCTATAGAAGTTGCGCAACCTCACCACATCTG 270
Qy 53 PhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyr 72
Db 271 CTCATTGCCAACCTGGCCATCTCGACTTCTTGGTGGCCATCATCTGCTGCCCTTCGAG 330
Qy 73 IleProHisValLeu-----PheAsnTrpAsnPheGlySerGlyIleCysMetPhe 89
Db 331 ATGGACTACTACGTGGTACGGCAGCTCTCTCGGAGCATGGCCACGCTGCTCTGT----- 384
Qy 90 TrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyr-----AsnIle 105
Db 385 ---GCCTCCGCTAACCTACCTGCGC---ACGCTCTCCCTCTACGCTCTCCACCAATGCCCTTG 438
Qy 106 ValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGln 125
Db 439 CTGGCCATTGCCATTGACAGATATCTCGCCATCGTTCACCCCTTCAAAACACCGATGAAT 498
Qy 126 HisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeu 145
Db 499 TATCAAAACGCCCTCTTCTCTGATCGCC-----TTGGTCTGGATGGTGTCTCATCTCTC 549
Qy 146 ValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrLysAsp 165
Db 550 ATTGC-CATCCATCGGCTTACTTTGC-----AACAGAAACCGCTCTCTTTAT 596
Qy 166 Cys---GluProGlyPheValThrGluTyrTrpIleLeuThrIle-----ThrMetLeu 182
Db 597 TGTCAAGAGCCAGGAGAAAGATCTTCTGTGGCCAGATCTTGTGGCTGTGGATCAGCAGCTCTA 656
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Qy 223 SerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGly 242
Db 766 -----
Qy 243 LeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeu 262
Db 781 TCTCCCGGAGCTCTGGTTCAAGCAGTCCCTGGGTCCACGAGC----- 828
Qy 263 ValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrp 282
Db 828 -----
Qy 283 Arg-SerGluSerAlaAlaLeu-ArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgL 302
Db 829 AGATTCCGCAAGCGCTGCGCTGCCGC-----AGGA 858
Qy 302 ValLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrC 322
Db 859 AGCGGTCTGGTCTGATGTCATCTCAGCGCTATGCTGCTGCTGGCACCCTTCT 918
Qy 322 ValLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerValTrpT 342
Db 919 ACGGTTTCCACCATGCTTCGTGACTTCTTCCC-----ACTGTGTTCTGTAAGGAAGCACT 975
Qy 342 YrSerIleAlaPheTrp-----LeuGlnTrpPheAsnSerPheValAsnProp 358
Db 976 ACCTCACTGCTTCTAGCTGGTGCAGTGCATCGCCATGAGCAACAGCATGATCAACACCG 1035
Qy 358 heLeuTyrProLeuCyHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValT 378
Db 1036 TGTGCTTCGTGACGGTCAAGAACCAACACCATGAAGTACTTCAAGAAGATGATGCTGTGC 1095
Qy 378 hrLysTrpProAlaLeuSerGlnAsnGlnSerValSerSer 391
Db 1096 ACTGGCGTCCC-----TCCAGCGGGGAGCAAGTCCAGT 1130

RESULT 14
US-11-312-958-23
; Sequence 23, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553.
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MPI02-027P1RNONMIM
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
```

```
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1105
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(1101)
US-11-312-958-23

Alignment Scores:
Pred. No.: 1.03e-10 Length: 1105
Score: 206.50 Matches: 74
Percent Similarity: 38.3% Conservative: 71
Best Local Similarity: 19.5% Mismatches: 129
Query Match: 10.1% Indels: 105
DB: 9 Gaps: 9

US-10-626-445-8 (1-391) x US-11-312-958-23 (1-1105)
Qy 11 ProProAlaAlaGlnValProLeuAlaPheLeuMetSerSerPheAlaPheAlaIleMet 30
Db 118 CCTCCCTGGGTGGCTCCAGCGCTGTCCGGGTGCTCATGCTCACCGCCGCGTGGACGTC 177
Qy 31 ValGlyAsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArgHisArgSer 50
Db 178 GTGGCAACCTCTCGTGGTGATCTCTCCGTGCTCAGGACCGCAAGCTCCGGAACGACGT 237
Qy 51 AsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIlePro 70
Db 238 AATTGTGTTCTTGTGAGCTGGCATTTGGCTGACCTGGTGGTGGCTTCTTACCCCTACCCG 297
Qy 71 LeuTyrIleProHisValLeuPheAsn---TrpAsnPheGlySerGlyIleCysMetPhe 89
Db 298 CTAATCTCTGTGGCCATCTTCTATGACGGCTGGGCGCTGGGCGGAGGACATGCAAGGCC 357
Qy 90 TrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSer 109
Db 358 AGCGCTTTGTATGGGCTGAGCGTTCATCGGCTCTGCTTCATATACATCAGTCCATCGCC 417
Qy 110 TyrAspArgTyrGlnSerValSerAsnAlaValSer-----TyrArgAlaGln 125
Db 418 ATTAACCGCTACTGTACTATCTGCCAGCATGTCCAGCATGCCATACCACCGAATCTACCGGCTGG 477
Qy 126 HisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeu 145
Db 478 CACACCCCTCTG-----CACATCTGCTCATCTGCTGCTCTCCTCCTCCTCCTCCTCCTCCT 522
Qy 146 ValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrLysAsp 165
Db 523 GCCTTGTGTCACCACTTCTTT-----GTGGGTCTCCTGGAG 558
Qy 166 CysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr----- 180
Db 559 TAGCACCACGCGCATCTATTCTGCACCTTCATCCAGACCGCCAGCAGCAGCAGCAGCAGCAG 618
Qy 181 -----MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGln 198
Db 619 GCAGTGGTGGTGCATCCATCTTCTCTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 678
Qy 199 IleTyrTrpSerLeuTrpLysArgAlaLeuSerArgCysProSerHisAlaGlyPhe 218
Db 679 ATCTGGGTGCTGGTGGTCTTACGGCCCGC----- 705
Qy 219 SerThrThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThr 238
Db 706 -----AGGAAA 711
Qy 239 SerAsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLys 258
Db 711 -----AGGAAA 711
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Db 712 GCCAAGCCA----- 720
Qy 259 SerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysVal 278
Db 721 GAGAGCAGGCTGGCTGAGACCCAGGACTTGGGAGCTTTCTAACCATGTTT----- 774
Qy 279 GlySerPheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeu 298
Db 774 ----- 774
Qy 299 ArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrp 318
Db 775 -----GTGGTGTGTGGATCTTTGGCATCTGCTGG 804
Qy 319 AlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLys 338
Db 805 GCTCCACTTAACATGCAFCGCGCTGGCTGGCCATCAACCCCAAGAAATGGCTCCCCAG 864
Qy 339 -----SerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsn 356
Db 865 ATCCCTCAGGGGTATTTGTCACTAGTACTTACTGGCTTATTTCAACAGCTGCCTGAAT 924
Qy 357 ProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu 375
Db 925 GCCATTGCTATGGGCTCTTGAACCAAACTTCGCGAGGAATACAAAGAGGATCCTC 981
RESULT 15
US-11-312-958-11
; Sequence 11, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22425, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MP102-027PIRNONMIN
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1727
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1272)
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US-11-312-958-11
Alignment Scores:
Pred. No.: 2,23e-10 Length: 1727
Score: 206.00 Matches: 77
Percent Similarity: 36.9% Conservative: 66
Best Local Similarity: 19.8% Mismatches: 147
Query Match: 10.1% Indels: 98
DB: 7 Gaps: 13

US-10-626-445-8 (1-391) x US-11-312-958-11 (1-1727)
Qy 19 AlaPheLeuMetSerSerPheAlaPheAlaIle-----MetValGlyAsnAlaVal 35
Db 214 GCCCTGCTCATTTGGCTTACTCTTTCATCATTTCTTCTTCTTCTTGGCAACGTCCTG 273
Qy 36 ValIleLeuAlaPheValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 55
Db 274 GTCTGTCTCATCTTTCAAGAACCCAGCAATGCACCTCGGCCACACGCTCTTTCATGTC 333
Qy 56 AsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIleProLeu---TyrIlePro 74
Db 334 AACCTGGCATTTGCCGACATAATGATCAGCTGTCTCAACACCCCTTCACTTGTGTCG 393
Qy 75 HisValLeuPheAsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAsp 94
Db 394 TTGTGTGAACAGCACATGGATATTTGGGAAGGCGCATGTGCCATGTCAGCCGCTTTGCC 453
Qy 95 TyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGln 114
Db 454 TACTGTCTCACTGCGACGCTCTGACGACTGCACAGCCATTGGGTGGATCGCCACGAG 513
Qy 115 SerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAla 134
Db 514 GTCATGACGACCCCTTGAAACCCCGG-----ATCTCAATCAACAAGGGTGTATC 564
Qy 135 GlnMetValAlaValTrpIleLeuAlaPheLeuValAsnGlyPrometIleLeuAlaSer 154
Db 565 TACATCGCTCATCTGGACCATGGCTACGTTCTTTTCACTCCACATGCTATGTCGAG 624
Qy 155 Asp-----SerTrpLysAsnSerThrAsn-----ThrLysAspCysGluProGlyPhe 170
Db 625 AAATATTATTACTTCAAAATACAGTAGGACATTTGTGGCTCCCTCTGCTGCCAGACTTC 684
Qy 171 ValThrGlu-----Trp---TyrIleLeuThrIleThrMetLeuLeuGluPhe 185
Db 685 CCGTAGCCAGCTGACCTCTTCTGGAGTAGTACCTGGACCTTGGCCACTTCACTCTCTAC 744
Qy 186 LeuLeuPro-----ValIleSerValAlaTyrPheAsnValGlnIleTyrTrpSerLeu 203
Db 745 ATCTGCGCCCTCTCATCATCTCTGTGGCTAC-----GCTCGTGTGGCCAGAAACTG 798
Qy 204 TrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThrThrSerSer 223
Db 799 TGG----- 801
Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
Db 802 -----CTGTGTAAT----- 810
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgLysSerSerIleLeuVal 263
Db 810 ----- 810
Qy 264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
Db 811 -----ATGATTGGCGATGTACCACA 831
Qy 284 SerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGlyArgLysLeu 303
Db 832 GAGCAGTACTTTGCCCTCGCGCGCAAAAG-----AAGAGAGACC 870
Qy 304 AlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeu 323
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